

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2001, 00:19:43 ; Search time 1440.11 Seconds

(without alignments)
10309.950 Million cell updates/sec

Title: US-09-510-332-2

Perfect score: 900
Sequence: 1 atgctagagcttcacccat.....acagtaagctcgtcagta 900

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sta: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_om: *
20: em_ov: *
21: em_ov: *
22: em_pat: *
23: em_ph: *
24: em_pl: *
25: em_ro: *
26: em_sta: *
27: em_sy: *
28: em_un: *
29: em_vl: *
30: em_hgo_hum: *
31: em_hgo_inv: *
32: em_hgo_inv: *
33: em_hcg_hum: *
34: em_hcg_inv: *
35: em_hcg_inv: *
36: em_hcg_inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	900	100.0	900	6	AX097696	AX097696 Sequence
2	900	100.0	900	6	AF227129	AF227129 Homo sapi
3	900	100.0	132953	9	AC003015	AC003015 Homo sapi
4	898.4	99.8	146296	9	AC026787	AC026787 Homo sapi
5	675.6	75.1	141747	2	AC034214	AC034214 Homo sapi
6	390.2	43.4	1008	10	AF227140	AF227140 Rattus no
7	390.2	43.4	1331	6	AX097772	AX097772 Sequence
8	388.6	43.2	1008	10	AF227149	AF227149 Mus muscu
9	388.6	43.2	1698	6	AX097836	AX097836 Sequence
10	124.4	13.8	957	6	AX097708	AX097708 Sequence
11	124.4	13.8	957	6	AF227133	AF227133 Homo sapi
12	124.4	13.8	173735	9	AC006518	AC006518 Homo sapi
13	124.4	13.8	190002	2	AC068649	AC068649 Homo sapi
14	123.2	13.7	939	6	AX097712	AX097712 Sequence
15	123.2	13.7	939	9	AF227135	AF227135 Homo sapi
16	119.8	13.3	930	6	AX097751	AX097751 Sequence
17	119.8	13.3	951	6	AX097700	AX097700 Sequence
18	119.8	13.3	951	9	AF227130	AF227130 Homo sapi
19	119.8	13.3	82419	9	AC004979	AC004979 Homo sapi
20	117.8	13.1	167869	9	AC073342	AC073342 Homo sapi
21	117.8	13.1	184034	2	AC024156	AC024156 Homo sapi
22	111.4	12.4	213278	2	AC018630	AC018630 Homo sapi
23	108.8	12.1	3775	6	AX097857	AX097857 Sequence
24	108.8	12.1	960	6	AX097746	AX097746 Sequence
25	107.8	12.0	179029	2	AC096625	AC096625 Homo sapi
26	107.2	11.9	903	6	AX097723	AX097723 Sequence
27	106.8	11.9	1103	6	AX097848	AX097848 Sequence
28	103.6	11.5	2567	6	AX097840	AX097840 Sequence
29	102	11.3	184034	2	AC024156	AC024156 Homo sapi
30	101.4	11.3	1316	6	AX097830	AX097830 Sequence
31	101.2	11.2	894	10	AF240766	AF240766 Rattus no
32	101.2	11.2	1304	6	AX097792	AX097792 Sequence
33	101	11.2	314700	2	AC018743	AC018743 Homo sapi
34	95.4	10.6	162380	2	AC018851	AC018851 Homo sapi
35	95.4	10.6	314700	2	AC018743	AC018743 Homo sapi
36	94.2	10.5	912	6	AX097719	AX097719 Sequence
37	94.2	10.5	912	9	AF227137	AF227137 Homo sapi
38	93.8	10.4	162380	2	AC018851	AC018851 Homo sapi
39	92.4	10.3	900	10	AF227141	AF227141 Rattus no
40	92.4	10.3	6532	6	AX097776	AX097776 Sequence
41	91.4	10.2	900	6	AX097704	AX097704 Sequence
42	91.4	10.2	900	9	AF227132	AF227132 Homo sapi
43	90.6	10.1	900	6	AX097748	AX097748 Sequence
44	90.6	10.1	930	6	AX097757	AX097757 Sequence
45	87.8	9.8	924	6	AX097714	AX097714 Sequence

ALIGNMENTS

RESULT 1

AX097696 LOCUS AX097696 900 bp DNA 30-MAR-2001

DEFINITION Sequence 2 from Patent WO0118050.

AX097696 ACCESSION AX097696

VERSION AX097696.1 GI:13514345

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

SOURCE

LOCATION/Qualifiers

1.900 /organism="Homo sapiens"

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Zuker,C.S., Adler,J.E., Ryba,N., Mueller,K. and Hoon,M.

Patent: WO 0118050-A 2 15-MAR-2001;

THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US) ; THE SECRETARY OF

THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)

```

/d_b_xref="taxon:9606"
/note="human T2R01, hGR01"
BASE COUNT      203 a      203 c      172 g      322 t
ORIGIN

```

Query Match	100.0%	Score 900;	DB 6;	Length 900;
Best local Similarity	100.0%	Pred. No. 7.4e-205;		
Matches 900;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

[illegible]

RESULT 2
AF227129

LOCUS	AF227129	900 bp	DNA	PRI	18-MAR-2000
DEFINITION	Homo sapiens candidate taste receptor T2R1 gene, complete cds.				
ACCESSION	AF227129				
VERSION	AF227129.1	GI:7262604			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 900) Adler,E., Hoon,M.A., Mueller,K.L., Chandrasekhar,J., Ryba,N.J. and Zuker,C.S.				
TITLE	A novel family of mammalian taste receptors				
JOURNAL	Cell 100 (6), 693-702 (2000)				
MEDLINE	20222571				
REFERENCE	2 (bases 1 to 900) Adler,E., Hoon,M.A., Mueller,K.L., Chandrasekhar,J., Ryba,N.J.P. and Zuker,C.S.				
AUTHORS	Direct Submission Submitted (21-JAN-2000) NIDCR, NIH, Bldg. 10 Room 1N106, 10 Center Drive, Bethesda, MD 20892, USA				
FEATURES	Location/Qualifiers				
SOURCE	1..900				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/chromosome="5"				
	/map="5p15.2"				
	1..19				
	1..900				
primer_bind	/note="g protein-coupled receptor. PCR-derived sequence; similar to an interval in BAC AC003015"				
CDS	/codon_start=1 /product="candidate taste receptor T2R1" /protein_id="AAF43902.1" /db_xref="GI:7262605" /translation="MBSHLIYFLPLANTIOPLGIFNGITVYVNGIDLIKRRKAPLDLSCLAVSRIFLQFLFYVNAVVFIFETIKCSANCAILLFINDELMLATWGVAVCAVSAVSRHPLFTWLKMRISKLVPMMLGSLVYMSFCVSHKRYAGMVPYFLKFFPESQDIOEDLEDAIOIESFVAFESVPLIFLEAVLLIFLSGRLRROMRNTVAGSRVVGSRNATIDEDLILSLFLFYFSCHMKVFLSSLKFIHRRIFLFLYIVIGIVPSGHSLLILNPNKQNAKKFELHRSCKQ" <1..>900				
mRNA	/product="candidate taste receptor T2R1"				
primer_bind	881..900				
BASE COUNT	203 a 203 c 172 g 322 t				
ORIGIN					
Query Match	100.0%; Score 900; DB 9; Length 900;				
Best Local Similarity	100.0%; Pred. No. 7,4e-205;				
Matches	900; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 atgctagagctccaccatcatatctctctctctgcagtgatacaattctctctg 60				
DB	1 ATGCTAGAGCTCCACCTCATATATATTCTCTTCTTCGACGATATCAATTCTCTGGC 60				
QY	61 atttcacacaatgagcatcatctgtggtagtgatgagcatctgacttgatccaagcacagaana 120				
DB	61 ATTTCACACAAATGAGCATCATCTGTGGTGGATGGCATGACCTTATCATCAGACAGAAAA 120				
QY	121 atgagtcgagctgagcctccctctctctgtctgtgcgagttccagaattcttcgagttg 180				
DB	121 ATGGTCGCGCTGGATCTCTCTTCTTCTGTGTGCGCAGTTTCTAGAAATTTTCTGCAAGTTG 180				
QY	181 ttcatctctctacgtaatgagttgattctctctcatagaaattcatcatgctgtctgcg 240				
DB	181 TTCACTCTCTACGTTAATGTGATGTGTTATCTTCATCAGAAATTCATCATGCTGTCTGGC 240				
QY	241 aattgtcgcaattctcttattatataaagaatcggaacttggctgtgcacatgagctcgagc 300				
DB	241 AATTGTGCAATTCTCTTATTATAAATGAATGGAACCTTGGCTTGCACATGAGGCTCGGC 300				
QY	301 gtttcctatttgccacaagttcacagcttcgacgcccacgtcttcattcgtatgagaaata 360				

Db	301	gTTTTCTATGTGGCCAAAGCTTGGCCAGCGTCCGTCACCCACTTTCATCTGGTTGAAGATG	360
Oy	361	aggatataccaagctcgtgtcccatgtaatgactcctggggtctctgtatatagtataagatt	420
Db	361	AGGATATTCACAGCTGCTGCCATGTGATGATCCCTGGGGTCTGTCTATATGTATCATATGATG	420
Oy	421	tgttgttccataagaataatgacaggggtttgtgtccatattcctctaagaanaatttttc	480
Db	421	TGTGTGTTTCCATATGCAAAATATGACAGGGGTTATGGTCCATATCTCTTAAGGAAATTTTTC	480
Oy	481	tcccaaatgtccacaattccaagaagaatacactgagctatacagatttctctttgt	540
Db	481	TCCCAATATGCCACATTTCAAAAAGAGATACACTGGCTATACAGATTTTCTCTTTGTT	540
Oy	541	gctgagctcagtgatgcaattgcttatcttcccttttgcgttttgcctcttgatttctct	600
Db	541	GCTGAGCTTCTCAGTGCCATGCTTACTTATCTCTTTTGGCTGTTTGTCTATATTTTCTCT	600
Oy	601	ctgggagagacacaccggcaaaatgagaacaacaagtgcggcagcagaggtctcctgcag	660
Db	601	CTGGGAGAGCACACCCGGCAATGGAACACAGAGCGCGGACACAGAGGTTCTTGAGG	660
Oy	661	ggtgaccccatcagcaggggtgtgtctgtatctctgtccttcctgataccttaacttctccac	720
Db	661	GGTGACCCCATCAGCGCGCTGTCTGTATCCCTGTCTCTTCGATCTCTTACTTCTCCAC	720
Oy	721	tgcataaataaagtttctctctctctcctcacaagttcacatcagaagttcatcttctg	780
Db	721	TGCATGATTAAGTTTCTCTCTCTCTTAAGTTTCAATCACAAGGTTTATCTTTCTG	780
Oy	781	tcttcatacctctgtgattgtgatabaacctctctgacactctcattcaatttagga	840
Db	781	TTCCTCATCTCTGTATGTGATATATACCTCTCTGACACTCTCATCTTATTAATTAGA	840
Oy	841	aatccataattgaaacaaatgcaaaaagtctccctccacagaatagtgctgtaagga	900
Db	841	AATCCTAATTAATTGAACAAATATGCAAAAAGTTCTCTCTCACAGTAAGTGTCTGACGTGA	900
RESULT	3		
LOCUS	AC003015	132953 bp	DNA
DEFINITION	Human BAC clone GSI-113H23 from 5p15.2, complete sequence.		
ACCESSION	AC003015		
VERSION	AC003015.1	GI:2547255	
KEYWORDS	HTG.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Euhayrola, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 132953)		
AUTHORS	Wamsley, P., Kramer, J., Elliott, G. and O'Brien, D.		
JOURNAL	The sequence of H. sapiens BAC clone GSI-113H23. Unpublished		
REFERENCE	2 (bases 1 to 132953)		
AUTHORS	Waterston, R.		
JOURNAL	Direct Submission Submitted (20-OCT-1997) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA		
REFERENCE	3 (bases 1 to 132953)		
AUTHORS	Waterston, R.		
JOURNAL	Direct Submission Submitted (03-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA		
REFERENCE	4 (bases 1 to 132953)		
AUTHORS	Waterston, R.		
JOURNAL	Direct Submission Submitted (04-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA		
COMMENT	----- Genome Center Center: Washington University Genome Sequencing Center Center code: WUGSC		

```

Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.edu
----- Summary Statistics -----
Center project name: HGS113H23
-----

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded or sequenced with an alternate
chemistry; an attempt was made to resolve all sequencing problems,
such as compressions and repeats; all regions were covered by
sequence from more than one subclone; and the assembly was
confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University School of
Medicine, St. Louis MO.

Mapping information for this clone was also provided by Dr. Michael
Lovett, Departments of Otorhinolaryngology, Molecular Biology and
Oncology, University of Texas Southwestern Medical Center, Dallas
TX.

SOURCE INFORMATION:
This clone is from the first BAC library from Genome Systems, Inc.
(http://www.genomesystems.com).
Cell line: lymphoblastoid
Haplotypes: two
VECTOR: pBelobAC
Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is GSI-330J10, 200 bp overlap.
Actual start of this clone is at base position 1 of GSI-113H23;
actual end is at 132953 of GSI-113H23.

This clone contains STS HSC022Y45 (MID:g1235481) and HS268ZD9
(MID:g4354585).

FEATURES
Source
This clone contains polymorphisms with GSI-330J10.
1. 132953
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="GSI-113H23"
/clone.lib="GSBAC1"
/map="5p15.2"
complement(20..194)
/rpc_family="L1"
195..358
complement(359..853)
/rpc_family="L1"
2903..2933
/rpc_family="L1"
complement(3640..3667)
/rpc_family="L1"
complement(3764..3788)
/rpc_family="L1"
complement(3820..4112)
/rpc_family="ALU"
complement(4322..4351)
/rpc_family="L1"
complement(4444..4464)
/rpc_family="L1"
complement(5046..5122)
/rpc_family="L1"

```

[illegible]

Db	49767	ATTTCACAAATGGCATCATTTGGTGGTGAATGGCAATTTGACTTGATACGACAGAAAA	49708
Qy	121	atggtcctcgcgtggaatctctcttctctgtctcgcgagttccagaattttctgcagttg	180
Db	49707	ATGGCTCCGCGTGGATCTCCTCTTCTTGTTGTCGGCAGTTTCTAGAAATTTTCTGCAGTTG	49648
Qy	181	ttcatctcttaagtaaatgtaattgttatctctctctcacaagaattcaatgltgtctcg	240
Db	49647	TTTCATCTCTACGTTAAATGTGAATTTTATCTTTCATAGAAATTCATCATATGTCTCCG	49588
Qy	241	aattgtcaatctctcttaattaagaatgtgaacttgcctgcacaaatgagtcggc	300
Db	49587	AATGTGGCAATTCCTTTAATTAATGAATATGGAACTTTGGCTTGCACATAGCTCGGC	49528
Qy	301	gtttcctatgttgcacaaggttgcacggtccgcaaccactctcaatcgtgtgaagtg	360
Db	49527	GTTTTCTATTTGGCCAAAGTTTGGCCGCGCTCCATCCACCACCTTCATCTGATCGTTGAAGATG	49468
Qy	361	aggatataccaagctgtgtcccaatgagttgctcgggtctctgcataatgatactatgct	420
Db	49467	AGGATATCCAAAGCTGTGCCATGATGATCCTGGGGTCTGTGCTAATGATATCTATGATT	49408
Qy	421	tgtgtttccatagcaaatatgacaggttctatgtgtccataactctctaaggaaattttc	480
Db	49407	TGTGTTTCCATAGCAAAATATGACAGGGTTTATGTCCTCATCTTCTAAGAAATTTTTC	49348
Qy	481	tcccaaatgtccacatctcaaaaagaataacactggtctatacagaattttctcttgtc	540
Db	49347	TCCCAAAATGGCCAAATTCAAAAAGAAATACACTGGCTATACAAATTTTCTCTTTGCTT	49288
Qy	541	gctgagttctcagtgcaattgctaactctctcttctgtctgttgcctctgattctcct	600
Db	49287	GCTGAGTTCTCAGTGCATTCCTTAATCTTCCCTTTTGGCTGTTTTCCTTGAATTTTCTCT	49228
Qy	601	ctggggagggacacccggcaaatgagaacaacagtgtgcgcgcagcagaaggtttctctgcag	660
Db	49227	CTGGGGAAGGCACACCCGGCAATGAGAAACACAGTGGCGGCGACGAGGGTTCTCGGCAGG	49168
Qy	661	ggtgaccccatcagcggttgcgtgtctactctctgtccctccgaatcccttactctccac	720
Db	49167	GGTGACCCCATCAGGGGCTTCTGCTGTATCTCTGTCCTTCTTGATCTTACTTCTCCAC	49108
Qy	721	tgcataataaagttttctctctctctcctaagaatttcacatcaagaagttcatcttctg	780
Db	49107	TGCATGATAAAGTTTCTCTCTCTCTCTAAAGTTTCACATCAGAAAGGTTTCATCTTCTG	49048
Qy	781	ttcttcacctctggaattggtgataaacctctctggaactcttcacatcttaatttggga	840
Db	49047	TTCTTTCATCTTGTGATTGGATTAATCCCTTCTGGACACTCTTCATCTTAAATTTTACGA	48988
Qy	841	aatcctaaattgaaacaatatgcacaaaagttctctccctcacaagtaagtgtgcagtga	900
Db	48987	AATCCTAAATTGAAACAAATATGCAAAAAAGTTCCCTCCACAGTAAGTGTGTACAGTA	48928
RESULT: 5			
AC034214			
LOCUS			
DEFINITION			
AC034214 Homo sapiens chromosome 5 clone CTD-2001E22, WORKING DRAFT			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			


```

VERSION      AF227140.1 GI:7262626
KEYWORDS
SOURCE
ORGANISM      Norway rat.
               Rattus norvegicus
               Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
               Rattus.
REFERENCE
AUTHORS      1 (bases 1 to 1008)
               Adler, E., Hoon, M.A., Mueller, K.L., Chandrashekar, J., Ryba, N.J. and
               Zuker, C.S.
TITLE        A novel family of mammalian taste receptors
JOURNAL      Cell 100 (6), 693-702 (2000)
MEDLINE
REFERENCE    2 (bases 1 to 1008)
               Adler, E., Hoon, M.A., Mueller, K.L., Chandrashekar, J., Ryba, N.J. P.
               and Zuker, C.S.
TITLE        Direct Submission
JOURNAL      Submitted (21-JAN-2000) NIDCR, NIH, Bldg. 10 Room 1N106, 10 Center
               Drive, Bethesda, MD 20892, USA
FEATURES
source
               Location/Qualifiers
               1..1008
               /organism="Rattus norvegicus"
               /db_xref="taxon:10116"
               1..1008
               /note="G protein-coupled receptor"
               /codon_start=1
               /product="candidate taste receptor T2R1"
               /protein_id="AAF43913.1"
               /db_xref="GI:7262627"
               /translation="MMEGHILFEFLVMVQEVTVGLVANGLIYVVAIDILMKKNAPL
               DLLFLCATSRILQILCTIFADQLPSIVRHLDFDNTFVILINELSPETWLGVE
               YKATATIPHPFLMLKRRISLVPMLIGSLYIYITFHISRETSALIKPTLSLE
               PKNATQVGHAFTLSVLGLTLPFLFVAVLLIYSLMNSROMRTMGTRREYSG
               HAHISAMLSILFLILYSHVAVAILISQVYLISREYFCLAVIGMPSIHSIYLI
               LGNPLIKRNAMKFIYHCKCHCTRAMVTSRSPSLDLPVPTHPANKTSCSEACIMP
               S"
BASE COUNT   233 a 236 c 205 g 334 t
ORIGIN
Query Match 43.4%; Score 390.2; DB 10; Length 1008;
Best Local Similarity 66.2%; Pred. No. 5,6e-83;
Matches 595; Conservative 0; Mismatches 298; Indels 6; Gaps 2;

```

```

Db 421 ACTTTCAATCCATAGACAGACAGACTTGCAGAAATCTTAACCAATTTTATTAAGCCTTTT 480
Qy 481 tcccaaatgcccaatcacaagaagatacctgctatcacagatttctcttgc 540
Db 481 CTTAAAAATG---CAACTCAAGTCGGAACAGGCGATGCCACTACTCTCAGTCCTGTC 537
Qy 541 gctgaatcctcagtgccatcctatcctctcttcttgcgcttgcctgatttctc 600
Db 538 CTTGGGCTCACACTGCCGTTGTCATCTTACTGTTGCTTCTGCTTCTGATATATCTCC 597
Qy 601 ctgggagagacacacccgcaaatgagaacacagtgccgagcagaggtctcgcag 660
Db 598 CTGTGGAATATATAGACAGCAGATGAGACTA---TGCTAGACACAGGAGATATAGCGGA 654
Qy 661 ggtgacccatcagcggtgctgctatcctgcttctcctctctctctctctc 720
Db 655 CATGCTCACATCAGTGCAGAAATGCTCATCTTCAATCTCAATCCTATCTCTCCAC 714
Qy 721 tgcataataaagtttctctctctcctcctaagtttcaatcagaaggttcattctc 780
Db 715 TACATGGTGGCTGTCTGATCTACTCAAGTCTCTACTTGGAAACAGACCTTTGTA 774
Qy 781 tcttcattccttgatgtgatatataccctctgcacactctcattcaattttaga 840
Db 775 TTCTGCTTACTGTTATGTTGATGATGATGATGATGATGATGATGATGATGATGATG 834
Qy 841 aatcccaatgagaacaaatgcaaaaagttctctctccacagtaagtcgctcag 899
Db 835 AATCTTAAGCTGAACGAATGCAAAAAGTTCAATGTCATGTTAGTTGTTGTTGTTGTTG 893

RESULT 7
AX097772 LOCUS AX097772 1331 bp DNA PAT 30-MAR-2001
DEFINITION Sequence 78 from Patent W00118050.
ACCESSION AX097772
VERSION AX097772.1 GI:13514400
KEYWORDS
SOURCE Rattus sp.
ORGANISM Rattus sp.
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 1331)
AUTHORS Zuker, C.S., Adler, J.E., Ryba, N., Mueller, K. and Hoon, M.
TITLE T2R taste receptor family
JOURNAL Patent: WO 0118050-A 78 15-MAR-2001;
          THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US); THE SECRETARY OF
          THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES
source 1..1331
        /organism="Rattus sp."
        /db_xref="taxon:10118"
        /note="rat T2R1, rGR1"
BASE COUNT 348 a 289 c 266 g 428 t
ORIGIN
Query Match 43.4%; Score 390.2; DB 6; Length 1331;
Best Local Similarity 66.2%; Pred. No. 5,7e-83;
Matches 595; Conservative 0; Mismatches 298; Indels 6; Gaps 2;

```


Db 197 ATGGCCCCGTTGATCTGCTTCTATTTTGGCTGGGAGACTTCTCGGATCATTTCTGACGTTA 256
 Qy 181 ttcctctctacgttaatgtatgtatctctctctacatagatcatcatgtgtctgcg 240
 Db 257 TGTATATTTGTTGGACATTTGCTATTTCTTTTGGGACACACACTTTATTTGAGAGAC 316
 Qy 241 aatctgcaaatc 300
 Db 317 AATATATACCTTTGCTTTTCATCATTAATGAACTGAGTGTGTTGGTACATGCTGCTG 376
 Qy 301 gttctctatctgtccaaaggtgtgcagcgctcgctcaaccatctctcaatctgttgaagt 360
 Db 377 GTTTTCTACTGTGGCAAGATTTGCTACCATTTCTCTCAACCCACTTTTGTGTGCTGAAGATG 436
 Qy 361 aggatccaaagctgtgtcccaatgtatgtatctctctgtgtctctctctctctctctct 420
 Db 437 AGGATATTCAGCTTTGCTTACCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 496
 Qy 421 tctgct 480
 Db 497 ACTTTTCATTCATACAGACAGACACTTTCAAGCAATTTTAAAGCTTTTAAAGCTTTT 556
 Qy 481 tcccaaaatctcacaatctcacaagaatacactgtctatcagaattctctcttctgt 540
 Db 557 CCTAAATAATG---CAACTCAAGTCGGAAACAGGCAATGCCACACTACTCTCAGTCTGCTG 613
 Qy 541 gctgaatctctcagaagctgtctctctctctctctctctctctctctctctctctct 600
 Db 614 CTTCGGCTTCACACATGCTGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 673
 Qy 601 ctgggaagagccacacccggaacaaatgagaacacagctggccgcaagaggtctctggcag 660
 Db 674 CTGTCGAATTTATAGACAGCAGATGAGACAT---TGTAGGACACAGCAGAGATAGACGGA 730
 Qy 661 ggtgacccaatcagcggtgtgtctctctctctctctctctctctctctctctctctccac 720
 Db 731 CATGCTCATCATCAGTCAATGCTGCTCATTTCTATCTATCTATCTATCTATCTATCT 790
 Qy 721 tgcattgataaagttct 780
 Db 791 TACATGCTGCTGCTTCTCTATCTCTATCTATCTATCTATCTATCTATCTATCTATCT 850
 Qy 781 tctctcactctctgtatgtatctctctctctctctctctctctctctctctctctctct 840
 Db 851 TTTCTGCTTACTGCTTATTTGTTATGATGACCCCTCAATACACTGATTTGTTAATTTAGCA 910
 Qy 841 aatctcaaatctgaaacaaatgcaaaatgctctctctctctctctctctctctctctct 899
 Db 911 AATCTTAAGCTGAACGAATATGCAAAATGTTTCATTTGTTGATGTTGTTGATTTG 969

 RESULT 8
 LOCUS AF227149 1008 bp DNA 18-MAR-2000
 DEFINITION Mus musculus candidate taste receptor T2R19 gene, complete cds.
 ACCESSION AF227149
 VERSION AF227149.1 GI:7262644
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE 1 (bases 1 to 1008)
 AUTHORS Adler, E., Hoon, M.A., Mueller, K.L., Chandrasekar, J., Ryba, N.J. and Zuker, C.S.
 TITLE A novel family of mammalian taste receptors
 JOURNAL Cell 100 (6), 693-702 (2000)
 MEDLINE 20222571
 REFERENCE 2 (bases 1 to 1008)
 AUTHORS Adler, E., Hoon, M.A., Mueller, K.L., Chandrasekar, J., Ryba, N.J. P. and Zuker, C.S.
 TITLE Direct Submission
 JOURNAL Submitted (21-JAN-2000) NIDCR, NIH, Bldg. 10 Room 1N106, 10 Center

FEATURES Drive, Bethesda, MD 20892, USA
 Location/Qualifiers
 source 1..1008
 /organism="Mus musculus"
 /strain="129/SvJ"
 /db_xref="taxon:10090"
 CDS 1..1008
 /note="G protein-coupled receptor"
 /product="candidate taste receptor T2R19"
 /protein_id="AA043922.1"
 /translation="MEGHLFLLVVOPLTVGLANGILVYVNAIDLIMKRAPL
 DLLFCLATRIILQDLIFAOQLSLVHTLFADVTFTYIINELSLMFAVLGF
 YCAKIAIPHPFLMKRLSRILPMLILSVYVYVTFEIHSEKSEPKQIFSE
 SKMTVRPAHATILSVFRLILPLIFIVAVILLISLMISROMRWGTRPSR
 HALVSAMLSLSEILILYLSHDWNAVILCTGGLHFGSTFRFCLIVGMYSLSIVLI
 LGNPKLRNKRTEIVHCKCHCARAWVTSNPRISLDLPVPAITHISAKTISCSECIWP
 S"
 BASE COUNT 224 a 252 c 209 g 323 t
 ORIGIN
 Query Match 43.2%; Score 388.6; DB 10; Length 1008;
 Best local similarity 66.1%; Pred. No. 1.3e-82;
 Matches 594; Conservative 0; Mismatches 299; Indels 6; Gaps 2;

 Db 1 atgtcagaagctcaccatcatatctctctctctctctctctctctctctctctctctg 60
 Qy 1 ATGATGGAAGGTCATATGCTCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
 Db 61 attctcaaatgcatcatctgt 120
 Qy 61 GCTTTGGCAATGGCGCTCATTTGCTGTTGTCAATGCGATCGACTTATCATGTGGAAGAA 120
 Db 121 atgtcccgctgtgacatct 180
 Qy 121 ATGGCCCACTGAGATCTCTCTTTTGGCTGGGAGACTCTCGATCATTTCTCAATG 180
 Db 181 ttcactctcagtttaagtgatgtatctctctctcagaatcatcatcatctgtctctgc 240
 Qy 181 TGTATATGTTTGCACACCTGGTGTATCTGTTGGTGAACACACGTTATTTGCTGAC 240
 Db 241 aattgtcaattc 300
 Qy 241 AATGTATACCTTTGCTATATTAATGAACGACGACTCTGTGTTGCCAATGCTTGTGCT 300
 Db 301 gttctctatctgtccaaaggtgtgcagcgctcgctcaaccatctctcaatctgttgaagt 360
 Qy 301 GTTTTCTACTGTGCCAATGCTTACATCTCCCTCACCCACTCTTCTGCTGCTGAAGATG 360
 Db 361 aggatccaaagctgtgtcccaatgtatgtatctctctgtgtgtgtgtgtgtgtgtgtgt 420
 Qy 361 AGGATATCCAGTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 Db 421 tctgct 480
 Qy 421 ACTTTTCATTCATACAGACAGACTTCAAGACTTCTTAAGCAATGTTATTAAGCTTTT 480
 Db 481 tcccaaaatctcacaatctcacaagaatacactgtctatcagaattctctcttctgt 540
 Qy 481 TCTAATAAT---ACAACTCGGGTCAAGACAGGCTATGCAACTCTCAGTCTTTTCTG 537
 Db 541 gctgaatctcagaagctgtatgtatctctctctctctctctctctctctctctctct 600
 Qy 541 TTTGGGCTTCACACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 597
 Db 597 CTGGGGAAGCACCAGCAGCAATGGAACACAGTGGCCGCAAGAGGTTCTCTCTCTCTCT 660
 Qy 598 CTGTGGAACACAGCGGCAAGATGAG---GACTATGCTGGGGAACATGGAACCTATGCA 654
 Db 654 ggtgacccaatcagcggtgtgtctctctctctctctctctctctctctctctctctccac 720
 Qy 654 TTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT

Db 655 CATGCCCTGTCAGTCATGCTCCATTTCTGTCATTCCTCATTCCTCTATCTCTCCCAT 714
 Oy 721 tgcataataaaatttctg 780
 Db 715 GACATGGTAGCTGTTGATGTATGATACCAAGAGCTCCACCTTGGAAGCAAGCACTTTGCA 774
 Oy 781 tttctg 840
 Db 775 TTCTGCTTATTGTTATGTTATGTTATGTTATGTTATGTTATGTTATGTTATGTTATGTTA 834
 Oy 841 aatcctaataatgaacaaatgaacaaatgaacaaatgaacaaatgaacaaatgaacaaatgaac 899
 Db 835 AACCTTAAGCTGAACAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAG 893

RESULT 9
 AX097836 1698 bp DNA PAT 30-MAR-2001
 LOCUS AX097836 Sequence 142 from Patent W00118050.
 DEFINITION AX097836
 ACCESSION AX097836
 VERSION AX097836.1 GI:13514466
 KEYWORDS
 SOURCE Mus sp.
 ORGANISM Mus sp.

REFERENCE 1 (bases 1 to 1698)
 AUTHORS Zuker,C.S., Adler,J.E., Ryba,N., Mueller,K. and Hoon,M.
 TITLE 12r taste receptor family
 JOURNAL Patent: WO 0118050-A 142 15-MAR-2001;
 THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US) ; THE SECRETARY OF
 THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)

FEATURES
 source location/Qualifiers
 1..1698

BASE COUNT 426 a 397 c 352 g 523 t
 ORIGIN

Query Match 43.2%; Score 388.6; DB 6; Length 1698;
 Best Local Similarity 66.1%; Pred. No. 1.4e-82;
 Matches 594; Conservative 0; Mismatches 299; Indels 6; Gaps 2;

Oy 1 atctcagaagctcactctactctactctctctctctctctctctctctctctctctctctg 60
 Db 515 ATGATGGAAAGCTATATGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 574
 Oy 61 atttccaaatgagcatcattgctgctgctgctgctgctgctgctgctgctgctgctgctg 120
 Db 575 GCTTGGCAATGGCTCANTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 634
 Oy 121 atggtccgcgtgagctcctg 180
 Db 635 ATGGCCCACTGATCTGCT 694
 Oy 181 ttcactg 240
 Db 695 TGTATTTGTTGTCACAGCTGGCTATTCCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 754
 Oy 241 aattgtgcaattctg 300
 Db 755 AATGTACCTTTGTTTACATTAATAAGCAAGTACCTCTGTTGTTGTTGTTGTTGTTGTTGTT 814
 Oy 301 gttttctattgtgcaaggttgcagcgtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcg 360
 Db 815 GTTCTTACTGTCGAAGTGTCTACACATCCCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 874
 Oy 361 aggatatacaagctgctcag 420
 Db 875 AGGATATCCAGGTGTGGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 934

Oy 421 tgtgttccatagcaaatatgcaaggtttatagttcccaactctcctaaggaattttc 480
 Db 935 ACTTTCATTCATACAGAGACTTCAAGAACTTCTTAAGCAAACTTTTAACCTTTT 994
 Oy 481 tcccaaatgccaacatccaataaagaatacaactgctatagatctctctctctg 540
 Db 995 TCTAAAT---ACAACCTGGGTCAGACAGCGCATCCACACACTCTAGCTTTGTC 1051
 Oy 541 gctgagttcagtgccattgctatctctctctctctctctctctctctctctctg 600
 Db 1052 TTGGGCTCACACTACCATTTCTCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1111
 Oy 601 ctggggagagacaccccgcaaatgaagaacagtgccgagcagcagcagcagcagcagcagc 660
 Db 1112 CTGTGGAACACAGCCGCGAGATGAG---GACTATGTTGGAACTAGGAACCTACAGCA 1168
 Oy 661 ggtgacccatcagcgcgtgtgtctatctctctctctctctctctctctctctctctg 720
 Db 1169 CATGCCCTGCTCAGTGCAGATGCTCTCATTCCTCATTCCTCATTCCTCATTCCTCATTC 1228
 Oy 721 tgcataataaaatttctg 780
 Db 1229 GACATGTTACTTCTGATCTGATCCCAAGGCTCCACCTTTGGAAGCAAACTTTGCA 1288
 Oy 781 tttctcattctgtgtatgtatataccctctctctctctctctctctctctctctctctg 840
 Db 1289 TTCTGCTTATTGTTATGTTATGTTATGTTATGTTATGTTATGTTATGTTATGTTATGTTA 1348
 Oy 841 aatcctaataatgaacaaatgaacaaatgaacaaatgaacaaatgaacaaatgaacaaatgaac 899
 Db 1349 AACCTTAAGCTGAACAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAG 1407

RESULT 10
 AX097708 957 bp DNA PAT 30-MAR-2001
 LOCUS AX097708 Sequence 14 from Patent W00118050.
 DEFINITION AX097708
 ACCESSION AX097708
 VERSION AX097708.1 GI:13514358
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 957)
 AUTHORS Zuker,C.S., Adler,J.E., Ryba,N., Mueller,K. and Hoon,M.
 TITLE 12r taste receptor family
 JOURNAL Patent: WO 0118050-A 14 15-MAR-2001;
 THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US) ; THE SECRETARY OF
 THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)

FEATURES
 source location/Qualifiers
 1..957

BASE COUNT 258 a 202 c 192 g 305 t
 ORIGIN

Query Match 13.8%; Score 124.4; DB 6; Length 957;
 Best Local Similarity 50.3%; Pred. No. 1.9e-19;
 Matches 451; Conservative 0; Mismatches 421; Indels 24; Gaps 5;

Oy 1 atgctagaagctcaccatctactatctctctctctctctctctctctctctctctctctg 60
 Db 1 ATGGCAGATAAAGTGCAGACTTATTTGTTTACGAGTTGAGAGTTTCACTGGCG 60
 Oy 61 atttccaaatgagcatcattgctgctgctgctgctgctgctgctgctgctgctgctgctg 120
 Db 61 ATCTTAGGAAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
 Oy 121 atggtccgcgtgagctcctg 180


```

Db 601 TTTTTCCTTGACCTGCTCCCTCGGGAGACATATACGCAATGCACTGACGCCACA 660
Oy 640 ggcagcaggggttcctgcgaagggtgacacccacgcgcgtctgctgctatcgtcttc 699
Db 661 GCGTCACAGAGACCCGACAGAGCCCATGTCGAGAGCCCGAAGCGTCATTTCCCTTC 720
Oy 700 ctgctccctctctctcccatgcatgataaagtttctctctctctctctctctctac 759
Db 721 CTCTCCCTTTATGCTGCTATTTGCTCTCTCATTTGCCCTCAGCTCAGCTACTTATG 780
Oy 760 atcgaaggttcacctctctctctctctctctctctctctctctctctctctctga 816
Db 781 CCAGAGAGGATGATGCTGCTATTTGCTGTCAGTCATGCTTAATCTTACCTCAAGT 840
Oy 817 cactctcactcacttaatttaggaatcctaaatcgaacacaaatgaacaaagt 872
Db 841 CATTCATTATCTCAATAGTCTGGAGACAAATTAATTAAGACATGCTCTTAAGCT 896

```

```

RESULT 12
AC006518/c 173735 bp DNA PRI 01-MAY-1999
LOCUS Homo sapiens 12P13 BAC RPC111-144023 (Roswell Park Cancer Institute
DEFINITION Human BAC library) complete sequence.
ACCESSION AC006518
VERSION AC006518.17 GI:4713939
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

```

```

REFERENCE
AUTHORS Muzny,D., Areson,A.D., Bouck,J., Bunac,C., Chen,Z., Ding,Y.,
        Dugan,S., Durbin,J., Forcum,J., Garcia,C., Gorrell,J.H.,
        Gorrell,L.L., Hernandez,J., Issar,A., Jackson,L., Kneitz,S.,
        Kondejewski,N., Lau,S., Lee,E., Lee,R., Lichtenberg,O., Liu,W.,
        Logan,O., Lu,J., Marondel,I., Martinez,C., Merscher,S., Miller,A.,
        Montomery,K., Oswal,G., Pampell,L.R., Parish,B.J., Perez,L.,
        Rashid,N.D., Rives,C., Scherer,S.E., Shen,H., Shim,C., Simon,M.,
        Vo,Q., Williamson,A., Worley,K.C., Xiang,A.M., Yang,R., Yu,W.,
        Zhou,X., Kucherlapati,R., Nelson,D., and Gibbs,R.A.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 173735)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-1999) Molecular and Human Genetics, Baylor
        College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 173735)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (29-APR-1999) Human Genome Sequencing Center, Department
        of Molecular and Human Genetics, Baylor College of Medicine, One
        Baylor Plaza, Houston, TX 77030, USA
REFERENCE 4 (bases 1 to 173735)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-1999) Human Genome Sequencing Center, Department
        of Molecular and Human Genetics, Baylor College of Medicine, One
        Baylor Plaza, Houston, TX 77030, USA
COMMENT On Apr 29, 1999 this sequence version replaced gi:4589934.
        INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
        gc-help@bcm.tmc.edu

```

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as low coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT-----

```

----- Summary Statistics -----
Contig Length: 173735
Phrap values in estimate: 167393
Average error rate (BCM-Phrap estimate): 0.000263256
Fraction of Phrap values less than 40 : 0.0395058
Number of consensus changing edits: 3
Number of N's in consensus : 0

```

```

----- Consensus changing edits -----
Position Original+Context Edited+Context
31176 gtggggcggg(n)agaggggag gtgggctggg(9)gaggggagag
31177 tggggcggg(n)agaggggag tggggcggg(9)gaggggagag
104155 gagttcact(n)gtgttcctc gagttcact(c)gtgttcctc

```

----- Distribution of Quality < 40 Bases -----

# bases	5	10	15	20	25	30	35	40
1000	*	*	*	*	*	*	*	*
900	*	*	*	*	*	*	*	*
800	*	*	*	*	*	*	*	*
700	*	*	*	*	*	*	*	*
600	*	*	*	*	*	*	*	*
500	*	*	*	*	*	*	*	*
400	*	*	*	*	*	*	*	*
300	*	*	*	*	*	*	*	*
200	*	*	*	*	*	*	*	*
100	*	*	*	*	*	*	*	*
0	*	*	*	*	*	*	*	*

Phrap Value Range

FEATURES

SOURCE

Version: 1.01 gxf.

Location/Qualifiers

1. 173735

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="RPC111-144023"

/chromosome="12p13"

1873. 1957

/rpt_family="MER53"

repeat_region

```
repeat_region complement(2985..3277)
/rpt_family="Alusp"
repeat_region 6833..6962
/rpt_family="Alusg/x"
repeat_region complement(10209..10241)
/rpt_family="AT_rich"
repeat_region 11652..11865
/rpt_family="MER80"
repeat_region complement(12233..12365)
/rpt_family="PLAM_C"
repeat_region complement(12644..12693)
/rpt_family="L1M4"
repeat_region 12968..13198
/rpt_family="MIR"
repeat_region 13335..13697
/rpt_family="MLT1A1"
repeat_region complement(13934..13975)
/rpt_family="AT_rich"
repeat_region 14232..14649
/rpt_family="L1M4"
repeat_region 14652..14742
/rpt_family="(TA)n"
repeat_region 15287..15421
/rpt_family="L2"
repeat_region 16053..16237
/rpt_family="L1MB5"
repeat_region 16238..16272
/rpt_family="u2"
repeat_region 16273..17683
/rpt_family="L1MB5"
repeat_region 18072..18210
/rpt_family="L1MA4A"
repeat_region 18679..18844
/rpt_family="L1M4"
repeat_region 18895..19193
/rpt_family="L1PA16"
repeat_region complement(19194..19232)
/rpt_family="AT_rich"
repeat_region complement(19658..20023)
/rpt_family="L1PB2"
repeat_region complement(20437..20931)
/rpt_family="L1MA5A"
repeat_region complement(25697..25720)
/rpt_family="AT_rich"
repeat_region 26549..26960
/rpt_family="L1M4"
repeat_region 27024..27268
/rpt_family="L1M4"
repeat_region 27269..27511
/rpt_family="MER46"
repeat_region 27793..28087
/rpt_family="AluJo"
repeat_region complement(28088..28123)
/rpt_family="(GA)n"
repeat_region complement(28124..28214)
/rpt_family="(TA)n"
repeat_region 28277..28381
/rpt_family="L1M4"
repeat_region 28368..28912
/rpt_family="L1M4"
repeat_region 28925..29052
/rpt_family="MLT1A1"
repeat_region 29201..29267
/rpt_family="Alus"
repeat_region complement(29508..29559)
/rpt_family="(TAA)n"
repeat_region complement(29560..29858)
/rpt_family="AluY"
repeat_region complement(30369..30398)
/rpt_family="AT_rich"
repeat_region 31146..31316
/rpt_family="L1PA2"
repeat_region 31857..32070
```

```
repeat_region /rpt_family="AluJo"
complement(32384..33480)
/rpt_family="L1MA5"
Query Match 13.8% Score 124.4; DB 9; Length 173735;
Best Local Similarity 50.3%; Pred. No. 2.e-19;
Matches 451; Conservative 0; Mismatches 421; Indels 24; Gaps 5;

OY 1 atgtcagagctccaccatcatatcttctctcctcgtgatacaattctctctg 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1481 ATGCACATATAAGTCAGACTACTTATTTGTTCTTACCACTTGAGAGCTT 1422
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 61 atttcacaatggcaltgltggtggtggaatgcaatgactgaltgcaagcaaga 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1421 ATCTTACGAAATGCATTTCAATTCGATTCGTAACTGATGCTGCAAGAGAAA 1362
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 121 atgctcgcgcgtggtcctctctctctctctctcgtcgtgactggaatttcgcagtg 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1361 ATTGCTTCATGTATTATTCCTCAAGCTGCTGCAATTCAGAAATTTGCTATTGTGC 1302
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 181 ttcactctcagctaaatgltgaltgltatctctctcctcagaatt-----catcagtc 232
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1301 GTATTAATTAATTAATTTGTTATTTGTTGCTATATTCACATATGTCACATGCTAA 1242
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 233 gttctgcgaatgltgcaatctctctctctctctctctctctctctctctctctc 288
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1241 GAATGAGAAATCATTTGACTTCTGCAACACTAATCATTTAACTATCTGTTTGA 1182
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 289 acatggtcgcgcgtttctctatctggtcgaagtgccagcgccgctcaccctctcagtc 348
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1181 ACGTCCCTCAGCATTTACTATTTCTTCAAGATGAGTATTTCTTTCACCCCTTTTCTC 1122
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 349 tggctggaatgagataaccagctggtcccaatggaatgcaatgcaatgcaatgcaat 408
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1121 TGGATGAGAGTGGAGAAATTCAGAGGTGATTTCTGATTTACTGAGGTGCTGTTCTC 1062
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 409 gtatctatgatttggct--ttccatgcaataatgcaaggttcatggtcccaactcc 466
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1061 TCTGTGTTTATTAGCTTCACAGCTGAGAAATTTGAACCTGATTCAGTTTGTGTG 1002
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 467 taaggaatattctcccaaatgcca-----caattcaagaagaatacaactgct 519
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1001 AAGGCAAGAGAGAAACAACTTAATCTTGAGTTGCAAGTAAATTAACCAATGCT 942
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 520 atacagattctctctctctctctctctctctctctctctctctctctctctctct 579
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 941 TCTACCAAGTTATTTCTCAACCTGCAAGCTGCTCCCTTTTGTGTGCTAATGCTC 882
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 580 gtttgcctctgattctctctctctctctctctctctctctctctctctctctctct 639
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 881 TTTTTCCTTGTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 822
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 640 ggcagcagaggttcctgaggggtgacccatcagcgtgctgctctctctctctctct 699
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 821 GGGTCAAGAGACCCAGCAGCAGAGCCATGTGAGAGCCCTGAAGCTGTATTTCTCTC 762
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 700 ctgactctcactctctcctcactcactcactcactcactcactcactcactcactcact 759
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 761 CTTCCTCTCTTATTTGCTTATTTGCTTATTTGCTTATTTGCTTATTTGCTTATTTG 702
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 760 atcagaaggttcaatctctctctctctctctctctctctctctctctctctctct 816
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 701 CCAGAGAGGAAATGCTGTGATTTTGTGTGATTCATTAATGCTTAATGCTTCAAGT 642
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 817 cactctcactcactcactcactcactcactcactcactcactcactcactcactcact 872
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 641 CATTATTTATTTACTGAGGAGAAATTAATTAATTAATTAATTAATTAATTAATTAAGT 586
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
AC068649 AC068649 190002 bp DNA HTG 17-JUL-2001
LOCUS Homo sapiens chromosome 12 clone RP11-377C14, WORKING DRAFT
DEFINITION
```


Db 137526 TTTTTCCTTGATGCTCTCCCTCGGAGACATATACAGGCAATGACGTCAGTCCACCA 137585
 Oy 640 ggaagcagggttcctgagaggtgacacacacacagcggtgctgctatcctcctc 699
 Db 137586 GCGTGCAGAGAGCCCGACAGAGCCCATCTGAGAGCCCGAAGAGTCTATTTCTTC 137645
 Oy 700 ctgctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 759
 Db 137646 CTTCCTCTCTTATTTGCTTACTATTTGCTTCTTCTCTCTCTCTCTCTCTCT 137705
 Oy 760 atcgaaggttcacatctctcctcctcctcctcctcctcctcctcctcctcct 816
 Db 137706 CCAGAGACGGAATTAAGCTGATTTTTCGTCAGTCATGCTTAATCTACCCCAAGT 137765
 Oy 817 cactctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 872
 Db 137766 CATTCAATTAATCAATTAATCAATTAATCAATTAATCAATTAATCAATTAAT 137821

RESULT 14

AX097712 939 bp DNA PAT 30-MAR-2001
 LOCUS AX097712
 DEFINITION Sequence 18 from Patent WO0118050.
 ACCESSION AX097712
 VERSION AX097712.1 GI:13514362
 KEYWORDS
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 939)
 ZUKER,C.S., ADLER,J.E., RYBA,N., MUELLER,K. and HOON,M.
 T2R taste receptor family.
 Patent: NO 0118050-A-18 15-MAR-2001.
 TITLE THE RECEPTORS OF THE UNIVERSITY OF CALIFORNIA (US) ; THE SECRETARY OF
 JOURNAL THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)

FEATURES
 SOURCE location/Qualifiers
 1..939
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /note="human T2R9, hGR9"

BASE COUNT 248 a 187 c 186 g 318 t
 ORIGIN

Query Match 13.7% Score 123.2; DB 6; Length 939;
 Best Local Similarity 49.2% Pred. No. 3.7e-19;
 Matches 419; Conservative 0; Mismatches 418; Indels 15; Gaps 3;

Oy 22 atcctctctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 81
 Db 22 AT 81
 Oy 82 gt 141
 Db 82 GACTAGTAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 141
 Oy 142 ctctctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 193
 Db 142 CTGATCAGCTTGGCCATTCAGAAATCTCTCTCTCTCTCTCTCTCTCTCTCT 201
 Oy 194 ttaatgt 253
 Db 202 TTTATGCT 261
 Oy 254 tcttct 309
 Db 262 GTCTGACATTTTGCCAAATTAATCAAGTCTCTGTTACTTCTGCTCAATCTCT 321
 Oy 310 tgt 369
 Db 322 TTTACTCAAGATAGCCCAATTAATTCAGCCCAATTTTCTCTGCTGAGCTTAAGATCAAC 381

Oy 370 aagctgtcccatgacatcctcctcctcctcctcctcctcctcctcctcctcct 429
 Db 382 AAGTCAATGCTGTGGATTTCTTCTGGGCTCTTCTTATCTTAAATTAATTAAGTTC 441
 Oy 430 catagcaaatatgacaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 489
 Db 442 AAGAAATATGATATGCTGATACCTTTTTCAAAGTCAATGATGAAGAAATTAAT 501
 Oy 490 gcccaatctcaaaaagaagatcacctgctatagatctcctcctcctcctcctc 549
 Db 502 AAATTCAAAGTCAATTAATTAATTCAGTACTTTTCAACAGTTAACTGAACTGGGCTG 561
 Oy 550 tcaatgtcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 609
 Db 562 ATGTTCTCTTATTCCTTTTGGCTGATCTATTTCTTGTACTTCTTCTCTCTCT 621
 Oy 610 cacacccgcaaatgagaacacagctggtcgagcagaggtctcctgagaggtgaccc 669
 Db 622 CACACCAAGCAGATTCGACTGCTACAGCTGCTACAGAGAGCCCACTACAGAGCCCA 681
 Oy 670 atcagcggt 726
 Db 682 ATGAGGCGCATTAAGCGCAGTATCATCTTCTGCTCTCTCTCTCTCTCTCTCTCT 741
 Oy 727 ataaagttctcctcctcctcctcctcctcctcctcctcctcctcctcctc 786
 Db 742 TTTCTGTTATGACCTCTACGCGCTGATTTCTCTCAGGGAATTAAGTTGATGAT 801
 Oy 787 atcctgt 846
 Db 802 GACATAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 861
 Oy 847 aatgtgaacaa 858
 Db 862 AAGTTGAGGGA 873

RESULT 15

AF227135 939 bp DNA PRI 18-MAR-2000
 LOCUS AF227135
 DEFINITION Homo sapiens candidate taste receptor T2R9 gene, complete cds.
 ACCESSION AF227135
 VERSION AF227135.1 GI:7262616
 KEYWORDS
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 939)
 ADLER,E., HOON,M.A., MUELLER,K.L., CHANDRASHEKHAR,J., RYBA,N.J. and
 ZUKER,C.S.
 A novel family of mammalian taste receptors

JOURNAL

20222571
 Cell 100 (6), 693-702 (2000)

MEDLINE

2 (bases 1 to 939)
 ADLER,E., HOON,M.A., MUELLER,K.L., CHANDRASHEKHAR,J., RYBA,N.J. P.
 Direct Submission
 Submitted (21-JAN-2000) NIDCR, NIH, Bldg. 10 Room 1N106, 10 Center
 Drive, Bethesda, MD 20892, USA

JOURNAL

Location/Qualifiers
 1..939
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="12"
 /map="12p13"

FEATURES

source
 primer_bind
 1..19
 1..939
 /note="G protein-coupled receptor; PCR-derived sequence;
 similar to an interval in BAC AC006518"
 /codon_start=1
 /product="candidate taste receptor T2R9"

Tue Dec 11 09:54:24 2001

us-09-510-332-2.rge

Page 16

Result No.	Score	Query Match	Length	DB	ID	Description
1	900	100.0	900	22	AAF92502	Human T2R01 nucleoc
2	390.2	43.4	1331	22	AAF92528	Rat T2R01 nucleoc
3	388.6	43.2	1698	22	AAF92560	Mouse T2R19 nucleoc
4	124.4	13.8	957	22	AAF92508	Human T2R07 nucleoc
5	123.2	13.7	939	22	AAF92510	Human T2R09 nucleoc
6	119.8	13.3	930	22	AAF92525	Human T2R33 nucleoc
7	119.8	13.3	951	22	AAH49506	Human GTP-binding
8	119.8	13.3	951	22	AAF92504	Human T2R03 nucleoc
9	108.8	12.1	3775	22	AAF92571	Mouse T2R30 nucleoc
10	108.6	12.1	960	22	AAF92523	Human T2R30 nucleoc
11	108.4	12.0	2655	20	AAZ20861	Polynucleotide seq

12	107.2	11.9	903	22	AAE99515	Human T2R15 nucle
13	106.8	11.9	1103	22	AAE92566	Mouse T2R25 nucle
14	103.6	11.5	2567	22	AAE92562	Mouse T2R21 nucle
15	101.4	11.3	1316	22	AAE92557	Mouse T2R16 nucle
16	101.2	11.2	1304	22	AAE92553	Rat T2R06 nucleot
17	94.2	10.5	912	22	AAE92513	Human T2R13 nucle
18	92.4	10.3	6552	22	AAE92530	Rat T2R03 nucleot
19	91.4	10.2	900	22	AAE92506	Human T2R05 nucle
20	90.6	10.1	900	22	AAE92552	Human T2R31 nucle
21	90.6	10.1	930	22	AAE92527	Human T2R37 nucle
22	89.4	9.9	1260	22	AAD05499	Human secreted pro
23	89.4	9.8	1122	22	AAD05335	Human secreted pro
24	87.8	9.8	924	22	AAE92511	Human T2R10 nucle
25	87.4	9.7	930	22	AAE92526	Human T2R36 nucle
26	87.2	9.7	930	22	AAE92509	Human T2R08 nucle
27	86.8	9.6	1354	22	AAE92558	Mouse T2R17 nucle
28	86.4	9.6	1482	22	AAE92556	Mouse T2R15 nucle
29	86.2	9.5	2887	22	AAE92559	Mouse T2R18 nucle
30	85.2	9.5	1339	22	AAE92550	Mouse T2R09 nucle
31	85	9.4	1371	22	AAE92551	Mouse T2R14 nucle
32	84.8	9.4	954	22	AAE92514	Human T2R11 nucle
33	84.4	9.4	936	22	AAE92532	Oligonucleotide D1
34	84.4	9.4	936	22	AAE92524	Oligonucleotide D1
35	84.4	9.4	936	22	AAE92527	Oligonucleotide D1
36	84.4	9.4	936	22	AAE92529	Oligonucleotide D2
37	84.4	9.4	936	22	AAE92562	Oligonucleotide D2
38	84.4	9.4	938	22	AAE92525	Oligonucleotide D1
39	83.8	9.3	910	22	AAE92503	Human T2R02 nucle
40	83	9.2	1199	22	AAE92554	Human T2R03 nucle
41	82.6	9.2	1759	22	AAE92543	Mouse T2R02 nucle
42	81.6	9.1	1374	22	AAE92542	Mouse T2R01 nucle
43	80.6	9.0	936	22	AAE92524	Oligonucleotide D1
44	80.6	9.0	936	22	AAE92525	Oligonucleotide D1
45	80.6	9.0	936	22	AAE92527	Oligonucleotide D1

ALIGNMENTS

```

RESULT 1
ID AAF92502 standard; DNA; 900 BP.
AC AAF92502;
DT 16-MAY-2001 (first entry)
DE Human T2R01 nucleotide sequence SEQ ID NO:2.
XX
XX Human; rat; mouse; T2R: taste receptor; G-protein coupled receptor;
XX taste transduction G-protein coupled receptor; identification; tongue
XX taste sensory neuron; taste cell; taste modulator; food;
XX taste signalling pathway; ds.
XX
XX Homo sapiens.
XX
XX WQ200118050-A2.
XX
XX 15-MAR-2001.
XX
XX 08-SEP-2000; 2000MO-US24821.
XX
XX 10-SEP-1999; 99US-0393634.
XX
XX 22-FEB-2000; 2000US-0510332.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Zuker CS, Adler JE, Ryda N, Mueller K, Hoon M;
XX
XX WPI: 2001-211396/21.
XX
XX P-FSDB; AAB87731.
XX

```

PT Nucleic acids encoding the T2R family of G-protein coupled taste
 PT receptors, useful for identifying taste modulators that can be used in
 PT food and pharmaceutical industries to customize taste, for e.g. to
 PS decrease the bitter taste of food -
 XX
 XX Disclosure; Page 160; 249pp; English.
 CC AAF92502 to AAF92572 represent nucleic acids which encode taste
 CC transduction G-protein coupled receptors designated T2R proteins.
 CC AAB87731 to AAB87824 represent T2R proteins, and AAB87825 to AAB87830
 CC represent T2R family consensus sequences from the present invention.
 CC The T2R proteins are taste modulators. The nucleic acids are useful as
 CC probes for the identification of taste cells, as the nucleic acids are
 CC specifically expressed in taste cells. They also serve as tools for the
 CC generation of taste topographic maps that elucidate the relationship
 CC between the taste cells of the tongue and taste sensory neurons leading
 CC to taste centres in the brain. The taste modulators are useful for
 CC pharmacological and genetic modulation of taste signalling pathways.
 CC Modulatory compounds comprising T2R proteins can therefore be used in
 CC food and pharmaceutical industries to customise taste, for e.g. to
 CC decrease the bitter taste of food or drugs.
 XX
 XX Sequence 900 BP; 203 A; 203 C; 172 G; 322 T; 0 other;

Query: Match 100.0%; Score 900; DB 22; Length 900;
 Best Local Similarity 100.0%; Pred. No. 3.1e-237;
 Matches 900; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgttagagcttcaccatattatcttcttcgtcagatatacaattctctcggg 60
 DB 1 atgttagagcttcaccatattatcttcttcgtcagatatacaattctctcggg 60
 QY 61 atttcacaaatgagcatatgtgtgtagaagcatctgcatcagacaaagaaaa 120
 DB 61 atttcacaaatgagcatatgtgtgtagaagcatctgcatcagacaaagaaaa 120
 QY 121 atggctcgcgtgagatctctctctctctctctctctctctctctctctctg 180
 DB 121 atggctcgcgtgagatctctctctctctctctctctctctctctctctctg 180
 QY 181 ttctg 240
 DB 181 ttctg 240
 QY 241 aatctgcaatctg 300
 DB 241 aatctgcaatctctctctctctctctctctctctctctctctctctctg 300
 QY 301 gttctctatctgctcgaaggttgcagcgtccgctcaccactctcatctggtgaagatg 360
 DB 301 gttctctatctgctcgaaggttgcagcgtccgctcaccactctcatctggtgaagatg 360
 QY 361 aggatatacgaagcgtgctcgaatgagatcccggtgctcgcatactgatactcagat 420
 DB 361 aggatatacgaagcgtgctcgaatgagatcccggtgctcgcatactgatactcagat 420
 QY 421 tgtgtttctcctatgacaaatgacaggttctatggtcccatctctcctaagaaaaattctc 480
 DB 421 tgtgtttctcctatgacaaatgacaggttctatggtcccatctctcctaagaaaaattctc 480
 QY 481 tcccaaaaatgacaaatctcaaaaagaagatacactgctcctaagaaattctctctgt 540
 DB 481 tcccaaaaatgacaaatctcaaaaagaagatacactgctcctaagaaattctctctgt 540
 QY 541 gctgaagcttcagatgctcgtctatctctctctctctctctctctctctctctctctc 600
 DB 541 gctgaagcttcagatgctcgtctatctctctctctctctctctctctctctctctctc 600
 QY 601 ctgggagagcacaaccgagcaaatgagaaacaagtgagcggcagcaggtctccctgagag 660
 DB 601 ctgggagagcacaaccgagcaaatgagaaacaagtgagcggcagcaggtctccctgagag 660

QY 661 ggtgaccatcagcgtgtgtctctatctctgtctctctctctctctctctctctccac 720
 DB 661 ggtgaccatcagcgtgtgtctctatctctgtctctctctctctctctctctccac 720
 QY 721 tgcataaaagttctg 780
 DB 721 tgcataaaagttctg 780
 QY 781 ttcttcatctctgtgattgatatatacctctcggacactctcactcattattttaga 840
 DB 781 ttcttcatctctgtgattgatatatacctctcggacactctcactcattattttaga 840
 QY 841 aatcctaattgaaacaaatgacaaagttccctccacagtaagtgctgcagtga 900
 DB 841 aatcctaattgaaacaaatgacaaagttccctccacagtaagtgctgcagtga 900

RESULT 2

AAF92528

ID AAF92528 standard; DNA; 1331 BP.

AAF92528;

16-MAY-2001 (first entry)

Rat T2R01 nucleotide sequence SEQ ID NO:78.

Human; rat; mouse; T2R; taste receptor; G-protein coupled receptor;
 taste transduction G-protein coupled receptor; identification; tongue;
 taste sensory neuron; taste cell; taste modulator; food;
 taste signalling pathway; ds.

Rattus sp.

W0200118050-A2.

15-MAR-2001.

08-SEP-2000; 2000WO-US24821.

10-SEP-1999; 99US-0393634.

22-FEB-2000; 2000US-0510332.

(REGC) UNIV CALIFORNIA.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Zuker CS, Adler JE, Ryba N, Mueller K, Hoon M;

WPI; 2001-211396/21.

P-PSDB; AAB8781.

Nucleic acids encoding the T2R family of G-protein coupled taste
 PT receptors, useful for identifying taste modulators that can be used in
 PT food and pharmaceutical industries to customize taste, for e.g. to
 PS decrease the bitter taste of food -
 XX
 XX Claim 51; Page 189; 249pp; English.

AAF92502 to AAF92572 represent nucleic acids which encode taste
 CC transduction G-protein coupled receptors designated T2R proteins.
 CC AAB87731 to AAB87824 represent T2R proteins, and AAB87825 to AAB87830
 CC represent T2R family consensus sequences from the present invention.
 CC The T2R proteins are taste modulators. The nucleic acids are useful as
 CC probes for the identification of taste cells, as the nucleic acids are
 CC specifically expressed in taste cells. They also serve as tools for the
 CC generation of taste topographic maps that elucidate the relationship
 CC between the taste cells of the tongue and taste sensory neurons leading
 CC to taste centres in the brain. The taste modulators are useful for
 CC pharmacological and genetic modulation of taste signalling pathways.
 CC Modulatory compounds comprising T2R proteins can therefore be used in
 CC food and pharmaceutical industries to customise taste, for e.g. to
 CC decrease the bitter taste of food or drugs.
 XX

Sequence 1331 BP; 348 A; 289 C; 266 G; 428 T; 0 other:

Query Match 43.4%; Score 390.2; DB 22; Length 1331;
Best Local Similarity 66.1%; Pred. No. 3, 2e-97;
Matches 595; Conservative 0; Mismatches 298; Indels 6; Gaps 2;

```

OY 1 atgctagagctcactcacttacttacttcttctctgacgtgataaattctcttgg 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 77 atgaggaaggaggaataactctctctctcttcttcttcttcttcttcttctt 136
OY 61 atttccaaatgacacacacacacacacacacacacacacacacacacacacac 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 137 gctctggcaaatggcctcatttcttcttcttcttcttcttcttcttcttctt 196
OY 121 atgctcgcctgacatctctctctcttcttcttcttcttcttcttcttctt 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 197 atgcccgcctgacatctcttcttcttcttcttcttcttcttcttcttctt 256
OY 181 ttcattcttaagttaagtatgtatgtatcttcttcttcttcttcttcttct 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 257 tctatatctgttgcacaaattgtctatctctcttcttcttcttcttcttct 316
OY 241 aattgtgcaattctcttacttataatgaattgaacttcttcttcttcttctt 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 317 aatattactcttcttcttcttcttcttcttcttcttcttcttcttcttct 376
OY 301 gttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 377 gttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 436
OY 361 aggaatcgaactgcttcttcttcttcttcttcttcttcttcttcttcttct 420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 437 aggaatcgaactgcttcttcttcttcttcttcttcttcttcttcttcttct 496
OY 421 tctgttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 497 acttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 556
OY 481 tcccaaatgacacacacacacacacacacacacacacacacacacacacac 540
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 557 ccttcaaatgacacacacacacacacacacacacacacacacacacacacac 613
OY 541 gctgagcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 600
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 614 ctgtgagcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 673
OY 601 ctgtgagcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 660
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 674 ctgtgagcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 730
OY 661 gctgagcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 720
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 731 ctgtgagcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 790
OY 721 tgcagatataaagcttcttcttcttcttcttcttcttcttcttcttcttct 780
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 791 tgcagatataaagcttcttcttcttcttcttcttcttcttcttcttcttct 850
OY 781 tctcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 840
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 851 tctcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 910
OY 841 aatcctaattgaaacaaatgaaacaaatgaaacaaatgaaacaaatgaaacaa 899
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 911 aatcctaattgaaacaaatgaaacaaatgaaacaaatgaaacaaatgaaacaa 969

```

RESULT 3

AA92560

ID AAF92560 standard; DNA; 1698 BP.

XX AAF92560;

```

XX 16-MAY-2001 (first entry)
DT Mouse T2R19 nucleotide sequence SEQ ID NO:142.
XX
DE Human; rat; mouse; T2R; taste receptor; G-protein coupled receptor;
XX taste transduction G-protein coupled receptor; identification; tongue;
XX taste sensory neuron; taste cell; taste modulator; food;
XX taste signalling pathway; ds.
XX
XX Mus sp.
XX
XX WO200118050-A2.
XX
XX 15-MAR-2001.
XX
XX 08-SEP-2000; 2000WO-US24821.
XX
XX 10-SEP-1999; 99US-0393634.
XX
XX 22-FEB-2000; 2000US-0510332.
XX
XX (REGC ) UNIV CALIFORNIA.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Zuker CS, Adler JE, Ryba N, Mueller K, Hoon M;
XX
XX WPI: 2001-211396/21.
XX
XX P-PSDB; AAB87813.
XX
XX Nucleic acids encoding the T2R family of G-protein coupled taste
XX receptors, useful for identifying taste modulators that can be used in
XX food and pharmaceutical industries to customize taste, for e.g. to
XX decrease the bitter taste of food .
XX
XX Claim 51; Page 231; 249pp; English.
XX
XX AAF92560 to AAF92572 represent nucleic acids which encode taste
XX transduction G-protein coupled receptors designated T2R proteins.
XX AAB87731 to AAB87824 represent T2R proteins, and AAB87825 to AAB87830
XX represent T2R family consensus sequences from the present invention.
XX The T2R proteins are taste modulators. The nucleic acids are useful as
XX probes for the identification of taste cells, as the nucleic acids are
XX specifically expressed in taste cells. They also serve as tools for the
XX generation of taste topographic maps that elucidate the relationship
XX between the taste cells of the tongue and taste sensory neurons leading
XX to taste centres in the brain. The taste modulators are useful for
XX pharmacological and genetic modulation of taste signalling pathways.
XX CC Modulatory compounds comprising T2R proteins can therefore be used in
XX food and pharmaceutical industries to customise taste, for e.g. to
XX decrease the bitter taste of food or drugs.
XX
XX
XX Sequence 1698 BP; 426 A; 397 C; 352 G; 523 T; 0 other:

```

Query Match 43.2%; Score 388.6; DB 22; Length 1698;
Best Local Similarity 66.1%; Pred. No. 9, 7e-97;
Matches 594; Conservative 0; Mismatches 299; Indels 6; Gaps 2;

```

OY 1 atgctagagctcactcacttacttacttcttcttcttcttcttcttcttcttct 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 515 atgaggaaggacacatagctcttcttcttcttcttcttcttcttcttcttctt 574
OY 61 atttccaaatgacacacacacacacacacacacacacacacacacacacacac 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 575 gctctggcaaatggcctcatttcttcttcttcttcttcttcttcttcttctt 634
OY 121 atgctcgcctgacatctcttcttcttcttcttcttcttcttcttcttcttct 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 635 atgcccgcctgacatctcttcttcttcttcttcttcttcttcttcttcttct 694
OY 181 ttcattcttaagttaagtatgtatgtatcttcttcttcttcttcttcttcttct 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 695 tctatatctgttgcacaaattgtctatctcttcttcttcttcttcttcttct 754

```

QY	241	aatgtagcgaatctcccaatcttaataatgtgatacgtgaacctgtgcgtgcgaacaatggctgcg	300
Db	755	aagtgtaacctctgtcctacatataaagcgaacctgagctctctgtgttcggcaaatgctgtgt	814
QY	301	gtcttcatactgtgcgaaggtgtgcgaagcgtccgltcaacccaatccttcacatcgtgtgaaga	360
Db	815	gtcttcatactgtgcgaagatgtgtcaacacacccccaacccatctctcgtggcgtgaaga	874
QY	361	aggaataccaaagctgtgtcccatgtgatacctcgggggtctctgtctatagtatactatgt	420
Db	875	aggaataccaaaggtgtgtgcatagtgcgtacccgtgacatcgtcgtgtgtatagttaact	934
QY	421	tgatcttcatactgcgaatactgacaggtttatagtgltcccaatacctcctaaggaattctc	480
Db	935	aacttcatactcatabgcagagaggaacttcagaactctccaaagcaaatcttataagctcttt	994
QY	481	tcaccaaaatgcgaacatltcaaaaaagaatacgaactgtgcatacagaatltctctctgt	540
Db	995	tcataaaat---acaactcgggtcagagacagcagatgcacacatactcagtcctgtc	1051
QY	541	gtcgtagttctcagatgtccatctgtctatactctcctcttctgttcgtctcttgatcttctc	600
Db	1052	cttggtgcatacacaactatctcactctcaactgtgtcgtctcgtctcgtctctgtctcc	1111
QY	601	ctggggggggagaccccgccgaacatggaagaacacagtggtgcggcagacaggttccgtgcag	660
Db	1112	ctgtggggaacacacgcgcgcgcgtgag---gactatggtgggaacatcaggaaacctgcaga	1168
QY	661	ggtagcaccacacagcgcgtgtcgtctcatalccgtcctccatccatccactactctccac	720
Db	1169	catgcctcgtcagtgagatgctctccatctcgtcatalccatccatccatccatccatccat	1228
QY	721	tgcgtgttaagaatttctctctctctctctcaagaatttcacatacagaaggtcactctctc	780
Db	1229	gaactgtgtagcgtgtcgtacatcgttacccaagcctccactcacttggagaagcaaccttgca	1288
QY	781	tctctcaccctctgtgattgtgtatataccctctcgtgacactcctccatcttaatttaaga	840
Db	1289	tctgccttatgtgttatgtgtatgtatccctcctcctcaactcgtatgtcttaatttaaga	1348
QY	841	aatcctaataatgaaacaaatgtcaaaaagaattcctccctccacagtaagtgtcgtcagt	899
Db	1349	aaccttaagcttgaaacgaatactgaaaaaacgtttcaatgttccaatgtgaagtgtcagt	1407
RESULT 4			
AA#92508			
ID	AA#92508 standard; DNA; 957 BP.		
XX	AA#92508;		
XX			
DT	16-MAY-2001 (first entry)		
XX			
XX	Human T2R07 nucleotide sequence SEQ ID NO:14.		
DE			
KW	Human: rat; mouse; T2R: taste receptor; G-protein coupled receptor; identification; tongue;		
KW	taste transduction G-protein coupled receptor; identification; tongue;		
KW	taste sensory neuron; taste cell; taste modulator; food;		
KW	taste signalling pathway; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	MO200118050-A2.		
XX			
PD	15-MAR-2001.		
XX			
PF	08-SEP-2000; 2000MO-US24821.		
XX			
PR	10-SEP-1999; 99US-0393634.		
PR	22-FEB-2000; 2000US-0510332.		
XX			
PA	(REGC) UNIV CALIFORNIA.		

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PT
XX
PT Zaker CS, Adler JE, Ryba N, Mueller K, Hoon M;
XX
DR WPI; 2001-211396/21.
XX P-PSDB; AAB87737.
PT Nucleic acids encoding the T2R family of G-protein coupled taste
PT receptors, useful for identifying taste modulators that can be used in
PT food and pharmaceutical industries to customise taste, for e.g. to
XX decrease the bitter taste of food -
XX
PS Disclosure; Page 165-166; 249pp; English.
XX
XX AAF92502 to AAF92572 represent nucleic acids which encode taste
XX transduction G-protein coupled receptors designated T2R proteins.
XX AAB87731 to AAB87824 represent T2R proteins, and AAB87825 to AAB87830
XX represent T2R family consensus sequences from the present invention.
XX The T2R proteins are taste modulators. The nucleic acids are useful as
XX probes for the identification of taste cells, as the nucleic acids are
XX specifically expressed in taste cells. They also serve as tools for the
XX generation of taste topographic maps that elucidate the relationship
XX between the taste cells of the tongue and taste sensory neurons leading
XX to taste centres in the brain. The taste modulators are useful for
XX pharmacological and genetic modulation of taste signalling pathways.
XX Modulatory compounds comprising T2R proteins can therefore be used in
XX food and pharmaceutical industries to customise taste, for e.g. to
XX decrease the bitter taste of food or drugs.
XX
XX Sequence 957 BP; 256 A; 202 C; 192 G; 307 T; 0 other;

Query Match	13.8%	Score 124.4	DB 22	Length 957
Best Local Similarity	50.3%	Pred. No. 2.56	24	
Matches 451	Conservative 0	Mismatches 421	Indels 24	Gaps 5
QY	1	atgcctagagctccacctatcatctctctctctctgcagctgatacaattctctctggg	60	
Db	1	atgcaagataaagtcagacactctattgtctctagcagctggaggtttccagtcggg	60	
QY	61	atttcacaaatgtgcacatctgtgtgtgtgaatgtgcattgtactgtatcaagcagaaga	120	
Db	61	actctagggaaatgcctcatctgtgatttggtaaaatcctgacgtgcggctcaagaagaggaa	120	
QY	121	atgctctgcgcgagactctctctctctctctctctctgcggagcttcagaaattttctgaa	180	
Db	121	attgcctccattgtattatcatcccaagaatcgcggccatccagaagatttgcattgtgc	180	
QY	181	tccactctctacgttaagtgatctgtatctctctctcatalagaatt-----catcag	232	
Db	181	gtaaactatagattgttttatattgtgtgcataaccagatgctatgcacatgtaaa	240	
QY	233	gtctcgcgaattgtgcattctctt-----atttataaatgaattvgaaacttgcgtcgc	288	
Db	241	gaaaatgaataatcatgtactctctctcgcagacatacaaaatcatttgcattcgtttgca	300	
QY	289	acatgcgcgcgggtttcttatattgtgcagaagctgtgcagcgctccgcacccaactctc	348	
Db	301	acctgcctcagaattctcatctctctctctccagaataagtaattctctccaccaactttcc	360	
QY	349	tgtctgaagaatgaggaataaccagaagcttggcccatgtgaatgcctctggggctctgtat	408	
Db	361	tggatcgaagctggagatttcgaacgggttgattcttccttgattctcaactcgggtctgc	420	
QY	409	gtatctatfgatttgcgtt--ttccatagcaaatatgcaggggtttatgtgtccactctcc	466	
Db	421	tcgtgttatattagcctctccagccactgagaatttcgaacgcgtgattcgaagtttgc	480	
QY	467	taaggaagaattttctcccaaaatgcga-----caattcacaagaagataacactgcgtc	519	
Db	481	aaggaagaagagaaacaaactaaactcgtggattgcagagatcaataaataaactcaaa	540	
QY	520	atacgaattctctcttctgtctgctgaagcttccatgagccattgcatctatctctcttgc	579	

Db 541 tctacaaagtattcttaaccctggcaacgctgcctcccttctgtgtgtcctaattgtcc 600
 QY 580 gttctgctctgattctctctctgaggagacacccggcaaatgagaacacagtgccc 639
 Db 601 ttcttcctctgactcctctcctctcgagagacatacagcgaaatgacgtcagccaca 660
 QY 640 ggcagcagggtctctgacgaggggtgcacccaatcagcgcggtgtgtctatcccttc 699
 Db 661 ggggtgcagagcccccacacaggaagccatgtgagagccctgaagcgtcatcttcctc 720
 QY 700 ctgactcctcaactctccacatgataaaagtcttctctctctcttaaaattcac 759
 Db 721 ctctctcttattatgctcactatctgtccttctcacttgccacctccagctattatg 780
 QY 760 atcgaaggtcatctctctgtctctcatcctgtgtatgtt---ataacctcttga 816
 Db 781 ccagagcagagatagctgtgattcttggtgagtcatagtcttaactaccctcaagt 840
 QY 817 cactctcatcttaatttttagaagaatcccaatgaatgaacaaatgcacaaagaat 872
 Db 841 catcattatcccaactactggtggaacataaattagaacatgcatctctaaagt 896

RESULT 5

AAF92510 standard; DNA; 939 BP.

AAF92510;

16-MAY-2001 (first entry)

Human T2R09 nucleotide sequence SEQ ID NO:18.

Human; rat; mouse; T2R: taste receptor; G-protein coupled receptor;
 taste transduction G-protein coupled receptor; identification; tongue;
 taste sensory neuron; taste cell; taste modulator; food;
 taste signalling pathway; ds.

Homo sapiens.

MO200118050-A2.

15-MAR-2001.

08-SEP-2000; 2000MO-US24821.

10-SEP-1999; 99US-0393634.

22-FEB-2000; 2000US-0510332.

(REGC) UNIV CALIFORNIA.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Zuker CS, Adler JE, Ryba N, Mueller K, Hoon M;

MPI; 2001-211396/21.

P-PSDB; AAB87739.

Nucleic acids encoding the T2R family of G-protein coupled taste

receptors, useful for identifying taste modulators that can be used in

food and pharmaceutical industries to customize taste, for e.g. to

decrease the bitter taste of food -

disclosure; Page 167-168; 249pp; English.

AAF92502 to AAF92572 represent nucleic acids which encode taste
 transduction G-protein coupled receptors designated T2R proteins.
 CC AAB87731 to AAB87824 represent T2R proteins, and AAB87825 to AAB87830
 CC represent T2R family consensus sequences from the present invention.
 CC The T2R proteins are taste modulators. The nucleic acids are useful as
 CC probes for the identification of taste cells, as the nucleic acids are
 CC specifically expressed in taste cells. They also serve as tools for the
 CC generation of taste topographic maps that elucidate the relationship

CC between the taste cells of the tongue and taste sensory neurons leading
 CC to taste centres in the brain. The taste modulators are useful for
 CC pharmacological and genetic modulation of taste signalling pathways.
 CC Modulatory compounds comprising T2R proteins can therefore be used in
 CC food and pharmaceutical industries to customise taste, for e.g. to
 CC decrease the bitter taste of food or drugs.

Sequence 939 BP; 248 A; 187 C; 186 G; 318 T; 0 other.

Query Match 13.78; Score 123.2; DB 22; Length 939;

Best Local Similarity 49.24; Pred. No. 5.2e-24;

Matches 419; Conservative 0; Mismatches 418; Indels 15; Gaps 3;

QY 22 atcattctctctgacagatcaattctctcttgatcttccaaatgacatc 81
 Db 22 atatatattatcttaattcgtcgtggaatgacaaagagatttgggaaatggattcat 81
 QY 82 ggggtggaatgagcattgactgacacagacagaaatggtccgctgacatc 141
 Db 82 gtactagtaactgacatgactgactcaaaagagatattccttgatgacatc 141
 QY 142 ctctctgtctgacagttctagaatttctcgcagttgtcatctctacg----- 193
 Db 142 ctgactcagcttggccactccacagatctgtctgtgtglaatatcatatgcttc 201
 QY 194 ttaatgagatgttatctctctcatagaaatcacaatgctgtctcgaattggaattc 253
 Db 202 ttatgtctctcttccaggtacataatgcaatagcgtcagaatgaacatgtgaatt 261
 QY 254 tctt---atttaaatgaattggaattggaattggtccacagtcggtcttctat 309
 Db 262 gtcgacatttgcacaaatcaatcaagctctgttactctcttcgcccagatctctat 321
 QY 310 tggcgaagtttgcagcgcgcgtaccacactctcatcgtgttgaatgagatacc 369
 Db 322 ttaactcaagatgaacataatatacgcaccacttcttctgtcgtgaagcctaagcaac 381
 QY 370 aagctgtcccatgagatcctcgtgggtctctgtctatagtatcatgattgtttc 429
 Db 382 aaggtcatgttgcagatctctctgtgggtctctctatccttaattatgagttcca 441
 QY 430 catagcaaatatgcaggtttatgtgtccatctctcaagaagaatttctcccaaat 489
 Db 442 aagaatgatatagtgtataccttcaagaatcagatgaagaagaacattactgtg 501
 QY 490 gccacaattcaaaagaagaatatacagtcatacagaatttcccttgtgtcgtgac 549
 Db 502 aaattcaaatgagtaaaattcaggttacttcaaacagttaacccctgaacctgggg 561
 QY 550 tcaatgcatgtcttactctcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 609
 Db 562 atgttcccttactccttcttgcgactcacttcttctgttacttcttcccaagttaga 621
 QY 610 cacaccggcaaatgagaacacagctgcccgcagagaggtctcggcaggggtgaccc 669
 Db 622 cacaccagcagatcagatgcatagtcagaggttcaagagaccagtaagagccac 681
 QY 670 atcagcgtgtgtgtctatcctcgtctcttcttcttcttcttcttcttcttcttct 726
 Db 682 atgaagcgaataaagcagatcacttcttcttcttcttcttcttcttcttcttcttct 741
 QY 727 ataaagtcttctcttcttcttcaagttcacatcagaaggtctcttcttcttcttct 786
 Db 742 ttctgttatgacctcagcgtctgactcctcaggaatattatgttgaatgtgt 801
 QY 787 atctctgtatgttatcacttcttgaacactctcacttcaatttgaagaatcct 846
 Db 802 gacatgtaactgtcatttccatcagacattcatcttaattatggaatagc 861
 QY 847 aaatgaacaa 858
 Db 862 aagttgaaggaa 873

Db 1663 gtaaccacgcttgcgaacttaataccttactctctgctgtatatttcttcttctta 1722
 Qy 592 attctctcttggaggacacccggcaaatggaacacagtgccggcgaaggtt 651
 Db 1723 atctgtcttcttggtaaacatctcaagaagatgcattcgaatgcaagaagatcccgat 1782
 Qy 652 cctggcaggggtgacaccatcagcggtgtgtctatctctgtcttccctcgatctctac 711
 Db 1783 tccaaccacgaaggtccacataaagcttgcgaacggtgacccctctctctgttattt 1842
 Qy 712 -----ttctccacatgcgatataaagtttctctctctctcaagtttccatcaga 765
 Db 1843 gctgttacttcttctgtcccaatcactgcgatgttggaaatttggaggaagctgtagaac 1902
 Qy 766 aggttcaacttctgtctctcattcctgtgtattgtatataccctctgacactcttc 825
 Db 1903 gaacctgtccatcagtcagcgaacactgacatctatataccctcattcattcattc 1962
 Qy 826 attcttaatttaggaatccttaattgaacaaatgcaaaaagttccctccacagtt 885
 Db 1963 atcccaatttgggaaagcaagaagctgaaacagaccccttcttggatttgtgtcagatt 2022
 Qy 886 aagtgctg 893
 Db 2023 aagtgctg 2030

RESULT 12
 AAF92515
 ID AAF92515 standard; DNA; 903 BP.
 AC AAF92515:
 DT 16-MAY-2001 (first entry)
 DE Human T2R15 nucleotide sequence SEQ ID NO:29.
 XX
 XX
 KW Human; rat; mouse; T2R; taste receptor; G-protein coupled receptor;
 KW taste transduction G-protein coupled receptor; identification; tongue;
 KW taste sensory neuron; taste cell; taste modulator; food;
 KW taste signalling pathway; ds.
 XX
 OS Homo sapiens.
 XX
 PN W0200118050-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 08-SEP-2000; 2000MO-US24821.
 XX
 PR 10-SEP-1999; 99US-0393634.
 PR 22-FEB-2000; 2000US-0510332.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Zuker CS, Adler JE, Ryba N, Mueller K, Hoon M;
 DR MPI: 2001-211396/21.
 DR P-PSDB: AAB87745.
 XX
 PT Nucleic acids encoding the T2R family of G-protein coupled taste
 PT receptors, useful for identifying taste modulators that can be used in
 PT food and pharmaceutical industries to customize taste, for e.g. to
 PT decrease the bitter taste of food -
 XX
 PS Disclosure: Page 172-173; 249pp; English.
 CC AAF92502 to AAF92572 represent nucleic acids which encode taste
 CC transduction G-protein coupled receptors designated T2R proteins.
 CC AAB87731 to AAB87824 represent T2R proteins, and AAB87825 to AAB87830
 CC represent T2R family consensus sequences from the present invention.
 CC The T2R proteins are taste modulators. The nucleic acids are useful as

CC probes for the identification of taste cells, as the nucleic acids are
 CC specifically expressed in taste cells. They also serve as tools for the
 CC generation of taste topographic maps that elucidate the relationship
 CC between the taste cells of the tongue and taste sensory neurons leading
 CC to taste centres in the brain. The taste modulators are useful for
 CC pharmacological and genetic modulation of taste signalling pathways.
 CC Modulatory compounds comprising T2R proteins can therefore be used in
 CC food and pharmaceutical industries to customise taste, for e.g. to
 CC decrease the bitter taste of food or drugs.
 XX
 SQ Sequence 903 BP; 237 A; 178 C; 171 G; 317 T; 0 other;

Query Match 11.9%; Score 107.2; DB 22; Length 903;
 Best local Similarity 48.9%; Pred. No. 1.3e-19;
 Matches 444; Conservative 0; Mismatches 443; Indels 21; Gaps 5;

Qy 1 atgctagaagctcactcattatatttcttcttgcagtgatacaatttctctgg 60
 Db 1 atgataacttctcaccatcatttctcattcattagtgatttcttctgg 60
 Qy 61 atttccaaatggcattgtgtgtgtaatgacattgatacgaagcaaaa 120
 Db 61 aatttgcataaggtctcacaagtggtglaaattccattgagtggtcagaagcaaaa 120
 Qy 121 atggctcggctgacatctcttcttctgtctgcaggttcataaatttctgcagttg 180
 Db 121 atctccttctgtgacaaattctcactgcctgcaggttcacaaagtgttctctgg 180
 Qy 181 ttcatcttcaagtt-----aattgattgtatctcttcataagaattcattat 232
 Db 181 gtaataattacattgtatgacacgttattgataccagtttcatatagtttaggata 240
 Qy 233 gtctcggaattgtgcaattctctatttataatgattggaac-ttggctgcaca 291
 Db 241 agaattcactatataatgcctggctgataccacattcagcactggtgtgact 300
 Qy 292 tggctcggcttcttctatcttgcacaggttgcagctccgcacacattcattcgtg 351
 Db 301 agctcagcattatttatttctcctaagattgcacatttcccaatttatttcttcac 360
 Qy 352 ttgaagaatgaggaataccaaagctggctccatgatactctggggtctctgataatga 411
 Db 361 ttaaaaagggaattaaagatgtcattcaggtgatactatgtggtcttctgtattttg 420
 Qy 412 tcatagttctgtgtttccatagcaaatatgcaggtttatgtgccatacttctaagg 471
 Db 421 gttgtcattcttctgtgtgtaaacatgacg-agagtaatgtaacaaagaataatgaag 479
 Qy 472 aaatttctcccaaaatgcacacattcaaaaagaatacaactggtcatacagatttcc 531
 Db 480 aaacgtgagttggagatcaaatg-----agatccgaacaccccttcaagatgaact 534
 Qy 532 tcttctgtcgtgaatctcagtgcaattgctatcttctcttctgtctgtctgtg 591
 Db 535 gtaaccacgcttgcgaacttaataccttactctgtccctgttattcttctgtctta 594
 Qy 592 atttctctctgggaggaacacccggcaaatgaaacacagtgccggcgaagaggtt 651
 Db 595 atctgtctcttctgtgtaaacatctcaagaatggaattcatalgcaagaagatcccgat 654
 Qy 652 cctggcaggggtgacaccatcagcggtgtgtctatctctgtcctcctcgatcctctac 711
 Db 655 tccaaccacgaaggtccacataaagcttgcgaacggtgacccctctctgttattt 714
 Qy 712 -----ttctccacatgcgatataaagtttctctctctcctaaagtttccatcaga 765
 Db 715 gctgttacttcttctgtcccaatcactgcgatgttggaaatttggaggaagctgtagaac 774
 Qy 766 aggttcaacttctgtctctcattcctgtgtattgtatataccctctggaactctctc 825
 Db 775 gaacctgtccatcagtcagcgaacactgacatctatatacacccttattcattcattc 834

CC specifically expressed in taste cells. They also serve as tools for the
CC generation of taste topographic maps that elucidate the relationship
CC between the taste cells of the tongue and taste sensory neurons leading
CC to taste centres in the brain. The taste modulators are useful for
CC pharmacological and genetic modulation of taste signalling pathways.
CC Modulatory compounds comprising T2R proteins can therefore be used in
CC food and pharmaceutical industries to customise taste, for e.g. to
CC decrease the bitter taste of food or drugs.

XX Sequence 1316 BP; 384 A; 226 C; 259 G; 447 T; 0 other;

Query Match 11.3%; Score 101.4; DB 22; Length 1316;
Best Local Similarity 47.5%; Pred. No. 5.9e-18;
Matches 411; Conservative 0; Mismatches 436; Indels 18; Gaps 3;

QY 47 aattctctcttgggaatttcacaaatgcatatctggtggtgaatgcatctgacttga 106
DB 225 aattctaaatggcatctcttggcaatlggaatcatalagcgtggtgaacataaaggacttgg 284
QY -107 tcaagcaacgaanaaatggtctccgtcgatctctcttcttctgtctgtcgagtcttagaa 166
DB 285 tcaagggaaggaaagatctcttcagtcgacagatccctcactgctctgcccacatcccaaga 344
QY 167 ttcttcgagatctgcatctctctacgttaatgtagtattgtaatctctctcatagaaatca 226
DB 345 tgcgactgtgtgttaataatagtaagtgtgtagataattgtgctttaccagacaat 404
QY 227 tcaatgtctctcgaaattgtgcaattctcttata-----aattgaattgg 274
DB 405 ggaatgactgatatgaagagatcgaatgaatcagacatgaatgaacaaatlcacacagagta 464
QY 275 aacttggtcttgcacagatggtcggtctctatgttgcgaagttgccaagctgcgtc 334
DB 465 gtctctgtgtcttcaaaagtcctcagcatcttatttcttcaagatagaacaaattttcca 524
QY 335 acccaactctcactcgtgtcgaagatgagataatccaagcttggcccatlgatgactcgtg 394
DB 525 accctatcttctcttaatttaaaagtcagacttaaaaaagtcagtataagacattgataa 584
QY 395 ggtctctgtctatagtatactatgatttgttcttcataatgcaaatatgcaaggttataig 454
DB 585 tgccttgaatctctcttcttgaatataatcattatgaatgcaccttgagaacattttaa 644
QY 455 tcccaacttccaaagaanaattttctccaaaatgccaatlcacaaagaagatacac 514
DB 645 tcaatgaataataatgatatctatgcttacaagcttgaatttgaataacacacagctttcta 704
QY 515 tggctatacagaatctctcttcttgttgcgtgagttctcagtgccatgtctatctctt 574
DB 705 tgcctgttcccatltgccaacacacatgttctgggttc--ataccttctgtctgtcctgg 761
QY 575 tttgcttcttgcgtctgatttctctctctggtgagggcacaccccgcaaatgagaacaacag 634
DB 762 tcaacttctgctctcttcttcttccctcgtggaacaacacagagaagaatgcaacaacagtg 821
QY 635 tggcggcgaagggttctctcgtgaggtgtgacccaacagcggttgcgtctatctcgt 694
DB 822 ccgatgtatgcagagatgccaagcctaagccacacacagacagccttcgacagacattgatcg 881
QY 695 ccttctctgactctacttctctccactgcatgaataaagtlttctctctctctctaaagt 754
DB 882 cctccctccctcctgattcattcttctctcctgtctcatgttaagaagtlttgagtgtctc 941
QY 755 ttacacatcagaaggatcattctctcttctctcatcctctgtagtggatata--tacccct 811
DB 942 tgccttctgagagaagacatctcgtcttltgatacacaaggttgcagaagaacagcttctcgt 1001
QY 812 ctggacactctcacttaatttcttagaataatcctaattgaaacaaatgcaaaaaagt 871
DB 1002 cagtgacatctcctgtgtcctgattcttgcgaatgtaagaatgagaaggtctctctctatg 1061
QY 872 tctctctccacagtaagtgctgtca 896

DB 1062 tatccctgtgctgaggtgacagca 1086

Search completed: December 11, 2001, 02:39:56
Job time: 5768 sec.

Tue Dec 11 09:54:24 2001

us-09-510-332-2.rng

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2001, 22:44:08 ; Search time 1381.63 Seconds

(without alignments)
6999.849 Million cell updates/sec

Title: us-09-510-332-2

Perfect score: 900
Sequence: 1 atgctagaggtcaccatc.....acagtaagtcgtcagtcga 900

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estlin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estov:*
8: em_estov:*
9: em_hic:*
10: gq_estl:*
11: gq_estl2:*
12: gq_hic:*
13: gq_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pin:*
18: em_gss_pro:*
19: em_gss_rtd:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	750.4	83.4	806	11	BG209561 RST29087
2	681	75.7	742	13	AQ308694 CTRBI-EI-
3	649	72.1	650	13	AQ316999 CTRBI-EI-
4	514.2	57.1	758	11	BG203110 RST22479
5	293	32.6	310	13	AQ277039 CTRBI-EI-
6	249.4	27.7	261	11	BG192000 RST11106
7	248.6	27.6	463	10	AA416581 AA416581
8	223.2	24.8	321	11	BG188332 RST7350
9	80.2	8.9	554	10	AL037695 DKEP5640
10	61.2	6.8	589	13	AQ103952 HS_3107_A
11	53.8	6.0	589	13	AQ590563 HS_5400_A
12	52.8	5.9	787	13	AZ739176 RPCI-24-1

C 13	48.4	5.4	1101	13	CNS00KX5	AL078382 Drosophila
C 14	47.6	5.3	399	11	N52978	N52978 yv30B01.S1
C 15	47	5.2	652	13	BH045040	BH045040 RPCI-24-3
C 16	46.6	5.2	399	11	H81901	H81901 yv78a04.s1
C 17	46.6	5.2	528	13	AQ719085	AQ719085 HS_5514_B
C 18	45.4	5.0	949	13	CNS04A1H	AL281906 Tetradon
C 19	45.2	5.0	878	13	CNS0187R	AL108993 Drosophila
C 20	44.4	4.9	656	13	A2416308	A2416308 Drosophila
C 21	42.8	4.8	928	13	CNS00DKY	AL216308 Drosophila
C 22	42.6	4.7	639	13	CNS0170D	AL071865 Drosophila
C 23	42.4	4.7	752	13	CNS0477G	AL108367 Drosophila
C 24	42.2	4.7	679	13	CNS0164V	AL127621 Tetradon
C 25	42.2	4.7	889	13	A2531644	AL106297 Drosophila
C 26	42.2	4.7	1034	13	CNS06M08	A2531644 ENTH537R
C 27	42	4.7	849	13	CNS06M08	AL05798 T3 end of
C 28	41.8	4.6	459	10	A2571816	A2571816 ENTHR06TR
C 29	41.8	4.6	943	11	BF530656	AA187386 zp69C02.r
C 30	41.8	4.6	997	13	CNS005TE	BF530656 602071951
C 31	41.6	4.6	780	10	BEG42964	AL060767 Drosophila
C 32	41.6	4.6	891	13	A2531629	BEG42964 Cr12.7.10
C 33	41.6	4.6	901	13	A2531629	A2531629 ENTHG32TF
C 34	41.6	4.6	928	13	CNS01119	AL099687 Drosophila
C 35	41.4	4.6	541	13	CNS04KUS	AL295309 Tetradon
C 36	41.4	4.6	809	13	CNS00A7H	AL054820 Drosophila
C 37	41.4	4.6	858	13	CNS010K6	AL099072 Drosophila
C 38	41.4	4.6	1004	13	CNS005PG	AL060507 Drosophila
C 39	41.2	4.6	518	13	A2374617	A2374617 IM0127F01
C 40	41.2	4.6	628	13	BH095829	BH095829 RPCI-24-2
C 41	41.2	4.6	784	10	AL525973	AL525973 AL525973
C 42	41.2	4.6	851	13	CNS009FC	AL053504 Drosophila
C 43	41.2	4.6	1092	13	CNS020K7	AL175696 Tetradon
C 44	41	4.6	224	10	BH130880	BH130880
C 45	41	4.6	498	13	AQ616191	AQ616191 HS_5148_A

ALIGNMENTS

RESULT 1
BG209561
LOCUS
DEFINITION RST29087 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG209561
VERSION BG209561.1 GI:13731248
KEYWORDS
SOURCE
ORGANISM Homo sapiens
human.
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Dahl, T., Thornton M., Ramachandran, R., Whittington, J., Lerner, L., Krishoc, D., McElligott, K., Clark, S., Mays, R., Smith, E., Veloso, N., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J., and Ducar, M.
TITLE Creation of Genome-wide Protein Expression Libraries using Random
JOURNAL Nat. Biotechnol. 19 (5), 440 (2001) In press
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scaine@atersys.com
High quality sequence stop: 557.
FEATURES
SOURCE
1. 806
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression',

Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 172 a 182 c 160 g 284 t 8 others

Query Match 83.4% Score 750.4; DB 11; Length 806;
Best Local Similarity 96.5% Pred. No. 9.7e-132;
Matches 763; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

45 acaattctctctggagatttcacaaatgacatcattggtggtgaatggcatgactt 104
14 ANNTTCTCTTGTGATTTTCACAAATGGCATCATGTGTGGTGAATGGCATGACTT 73
105 galcaagacagaaaaatggtcgtggtggtggtggtggtggtggtggtggtggt 164
74 GATCAAGCAGCAAGAAAAATGCCCTCGATCTCTTCTTCTTCTTCTTCTTCTTCT 133
165 aatttctctgagttgcatcctctctctctctctctctctctctctctctctct 224
134 AATTCTCTGCGATGTTGATCTTACGTTAATGATGATGATGATGATGATGATGAT 193
225 calcatgctctctgcaaatctgcaatctctctctctctctctctctctctctct 284
194 CATCATGTTGTTGCGAATGTGCAATCTCTTATTTAATGAAATGGAACTTGGCT 253
285 hgcacatggtcgtcgtggttctctctctctctctctctctctctctctctctct 344
254 TCCACATGCGCTCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 313
345 catctggttgaagaagaagataaccagcgtggtggtggtggtggtggtggtggt 404
314 CATCTGTTGAAAGATGAGATATCCAACTGTCCTCCATGAGATCTCTGCTGCT 373
405 atagatcatcatgatttctctctctctctctctctctctctctctctctctct 464
374 AATGTATCTATGATTTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 433
465 cctaaaggaaattctctcccaaaatgcccacaaatccaaaagaagaagaacgtgct 524
434 CCAAGCAAAATTTTCTCCCAAAATCCCAAAATTCAAAAGAGATACCTGCTATACA 493
525 gattct 584
494 GATTCTCTCTTGTGTCGAGATTCAGATGCTGCTATCTCTCTTCTTCTTCTTCT 553
585 gctcttgaattct 644
554 GCTCTTGAATTTACTACTGAGGAGGACACCCGCGCAATGAGAAACACAGTGGCG 613
645 cagggtct 704
614 CAGGCTTCTCTGCGAGGAGGACACCCGCGCTGCTGCTGCTGCTGCTGCTGCTG 673
705 cct 764
674 CCTCTACTCTCTCCACTGATGATGATGATGATGATGATGATGATGATGATGAT 733
765 aaggttcatct 824
734 AAGGTCATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 793
825 catcttaattt 835
794 CTCTTAATTTT 804

RESULT 2
LOCUS A0308694 742 bp DNA GSS 22-DEC-1998
DEFINITION CITBI-E1-253086.1F CITBI-E1 Homo sapiens genomic clone 253086, DNA

sequence.
ACCESSION A0308694.1 GI:4040728
VERSION A0308694.1
KEYWORDS GSS.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 742)
AUTHORS Adams, M.D., Rounsley, S.D., Zhao, S., Baas, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
TITLE Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
JOURNAL Unpublished (1998)
CONTACT: Shaying Zhao, William Nierman, Mark Adams
COMMENT Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@ligr.org
Clones are available from Research Genetics (Info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES
source
location/Qualifiers
1..742
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="253086"
/clone_1id="CITBI-E1"
/sex="male"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI; Caltech Human BAC Library D"

BASE COUNT 176 a 175 c 144 g 247 t
ORIGIN

Query Match 75.7% Score 681; DB 13; Length 742;
Best Local Similarity 100.0% Pred. No. 8.7e-137;
Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

220 gaattcatcatcgtct 279
2 GAATTCATCATGTTGTTGCGCAATTTGTCGAATTCCTTATTTATTAATGAATTTGA 61
280 tggcttgcccaatggtcgtggttctctctctctctctctctctctctctctctctct 339
62 TGGCTTGGCCACATGCTGCGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 121
340 cttctcatctgttgaagaatgagatgataccaaagctggtcccaatgagatgactggt 399
122 CTCTTCATCTGTTGATGAGATGAGATATCCAAAGCTGTCCTCATGATCTCTGGGCT 181
400 ctcgataatgataatgattctctctctctctctctctctctctctctctctctctct 459
182 CTGCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 241
460 taattctcaagaaattctctcccaaaatgcccacaaatcaaaaagaagatacactgct 519
242 TACTTCTCTAAGAAATTTTCTCCCAAAATGCGACAAATTCAAAAGAAATGATCACT 301
520 atcagagattct 579
302 ATACAGATTTTCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 361
580 gtttct 639
362 GTTTTGTCTTATTTTCTCTGCGGAGGACACCGCGCAATGAGAAACACAGTGGCC 421

0Y 640 ggcagcagggttcctgagcagggtgaccccatcagcgctgtctatctccttc 699
| | | | |
Db 422 ggcagcagggttcctgagcagggtgaccccatcagcgctgtctatctccttc 481
0Y 700 ctgacccctactctcccaacgacatgaataaagtttctctctctcctaagtttac 759
| | | | |
Db 482 ctgacccctactctcccaacgacatgaataaagtttctctctctcctaagtttac 541
0Y 760 atcagaaggttcaatctctctctctctctctctctctctctctctctctctc 819
| | | | |
Db 542 atcagaaggttcaatctctctctctctctctctctctctctctctctctctc 601
0Y 820 tctctccttaatttttgaggaatctcctaattgaacaataagtcctctc 879
| | | | |
Db 602 tctctccttaatttttgaggaatctcctaattgaacaataagtcctctc 661
0Y 880 cacagtaagtgctgcacgta 900
| | | | |
Db 662 cacagtaagtgctgcacgta 682

RESULT 3
A0316999 650 bp DNA GSS 22-DEC-1998
LOCUS CITBI-E1-2530B7.TF CITBI-E1 Homo sapiens genomic clone 2530B7, DNA
DEFINITION
ACCESSION A0316999
VERSION A0316999.1 GI:4040265
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 650)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Sub,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
JOURNAL Unpublished (1998)
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeel@igf.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21,
Class: BAC ends.

FEATURES
Location/Qualifiers
1..650
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2530B7"
/clone_lib="CITBI-E1"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"

BASE COUNT 149 a 152 c 125 g 224 t

ORIGIN
Query Match 72.1%; Score 649; DB 13; Length 650;
Best Local Similarity 100.0%; Pred. No. 6.9e-130;
Matches 649; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 220 gaattacatggtctgctggaattgcaattcttatttataaataatgaactt 279
| | | | |
Db 2 GAATTCATCATGTCGTCGCAATTCGCAATTCCTTATTATTAATGAATGCAACTT 61

0Y 280 tggcttccacatgctcgcggtttctctatgtgcgaagttgccagcgtccaccca 339
| | | | |
Db 62 TGGCTTGCCACATGCTCGCGGTTTCTATTGTGCCAAGTTGCCACGTCGCCACCCA 121
0Y 340 ctctcacatggttgaagatgaagatacccaagctgtgtccatgaatgatacctgggttc 399
| | | | |
Db 122 CTCTTCATCTGCTGAAGATGAGATATCCAAAGCTGTGCCATGATGATCTGGGCTCT 181
0Y 400 ctgctataatgataatgattgtgtgttccatagcaaatatgcaaggtttatgtccca 459
| | | | |
Db 182 CTGCTATATGATCTATGATGATTTGTTTCATATGCAATATGCAAGGCTTATGTGCCA 241
0Y 460 tactctcaaggaaattttctcccaaatgccaatctcaaatgaagaatacactgct 519
| | | | |
Db 242 TACTTCTTAAGAAATTTTCTCCAAAATGCCAATTTGAAAAGATATACACTGGCT 301
0Y 520 atacagaattctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 579
| | | | |
Db 302 ATACAGATTTTCTCTTTGTTGCTGAGATTTCTCACTGCTTATCTCTTTTGTCT 361
0Y 580 gtttgcctctgatttctctctctggtgagggacaccccgcaaatgagaaacagtggcc 639
| | | | |
Db 362 GTTTTGCTCTGATTTTCTCTGCGGAGGACACCCGCCAATGAGAAACACAGTGGCC 421
0Y 640 ggcagcagggttcctgagcagggtgaccccatcagcgctgtctatctccttc 699
| | | | |
Db 422 ggcagcagggttcctgagcagggtgaccccatcagcgctgtctatctccttc 481
0Y 700 ctgacccctactctcccaacgacatgaataaagtttctctctcctaagtttac 759
| | | | |
Db 482 ctgacccctactctcccaacgacatgaataaagtttctctctcctaagtttac 541
0Y 760 atcagaaggttcaatctctctctctctctctctctctctctctctctctctc 819
| | | | |
Db 542 atcagaaggttcaatctctctctctctctctctctctctctctctctctctc 601
0Y 820 tctctccttaatttttgaggaatctcctaattgaacaataagtcctctc 879
| | | | |
Db 602 TCTCTCATCTTATTATTAGGAATCTTAATTAATGAACCAATATGCAACTT 682

RESULT 4
BG203110 758 bp mRNA EST 21-APR-2001
LOCUS RST22479 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
DEFINITION BG203110
ACCESSION BG203110
VERSION BG203110.1 GI:13724797
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 758)
Hartington,J., J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Dahl,T., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Krashoc,D., McElligott,K., Clark,S., Mays,R., Smith,E.,
Velooso,N., Hess,J., Cochren,K., Lo,K., Offenbacher,J., Danzig,J.,
and Ducar,M.
TITLE Creation of Genome-wide Protein Expression Libraries using Random
Activation of Gene Expression
JOURNAL Nat. Biotechnol. 19 (5), 440 (2001) In press
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave. Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: sca@atersys.com
High quality sequence stop: 440.
FEATURES
Location/Qualifiers
1..758
/organism="Homo sapiens"
/db_xref="taxon:9606"

/clone.lib="Athersys RAGE Library"
 /cell_line="HT1080"
 /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
 BASE COUNT 184 a 169 c 165 g 240 t
 ORIGIN

Query Match 57.1%; Score 514.2; DB 11; Length 758;
 Best Local Similarity 95.8%; Pred. No. 7.3e-101;
 Matches 528; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

37 gcaagatatacaattctctctctggaatttcacaaatggcatcatgtggtggaatgac 96
 |||||||
 206 GCAGTATACATTTCTTCTGGATTTCACAAATGCAATCATGTGTGGTAAATGGC 265
 |||||||
 .97 attgactgataacagacagaaatgctcgcgtgatactctctctctctgctgca 156
 |||||||
 266 ATTGACTTGCATACACAGAAATGGCTCGCTGGATCTCTCTCTCTCTGCA 325
 |||||||
 157 gttctagaattctctgagtgctacatctctacgtaatgatactgatactctc 216
 |||||||
 326 GTTCTACAAATTTTCTGACATTTCTCATCTTAAATGATCTTATCTTCTTC 385
 |||||||
 217 atagaaatcaatcagtgctcggaaatgtaaatctctctctctataaagaattgaa 276
 |||||||
 386 ATAGAAATTCATGATGTCTGCAATGTGCAATCTTATCAATGAATGGA 445
 |||||||
 277 atttgatgacgaatgctgaggtctctctctctctctctctctctctctctc 336
 |||||||
 446 CTCTGCTTGGCCACATGCTGCGCTTTCTTATGTGCAAGCTTCCAGCTCCGTCAC 505
 |||||||
 337 ccactctcattcagtgctggaatgaaatgaaatcagtgctgctgctgctgctg 396
 |||||||
 506 CCACCTCTTATCTGCTGTAAGATGAGATATCCAGCTGCGCCCATGATGATCTGCTG 565
 |||||||
 397 tctctgataatgatactgatactgctctctctctctctctctctctctctctc 456
 |||||||
 566 TCTCTGCTTATGATCTTGTATGATTTGCTTCTCAATGCAATGATGCAAGGATATG 625
 |||||||
 457 ccactctcattcagtgctggaatgaaatgaaatcagtgctgctgctgctgctg 516
 |||||||
 626 CCATCTCTTCTTAAAGGACATTTCTCTCCCAAAATGCTCTATTCAAAGAACATACAC 685
 |||||||
 517 gctatacagaattc 576
 |||||||
 686 GCCATACACATTTTCT 745
 |||||||
 577 gctgctctgct 587
 |||||||
 746 GCTGTGATGCT 756
 |||||||

RESULT 5

LOCUS AO277039 310 bp DNA GSS 22-NOV-1998
 DEFINITION CITBI-EI-2516A7.TF CITBI-EI Homo sapiens genomic clone 2516A7, DNA sequence.

ACCESSION AO277039
 VERSION AO277039.1 GI:3903235
 KEYWORDS GSS

SOURCE

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 310)

REFERENCE

ADAMS, M.D., ROUNSLEY, S.D., ZHAO, S., BASS, S., LINHER, K., GOLDEN, K.,

BERRY, K., GRANGER, D., SUB, E., WIBLE, C., SHIZUYA, H., SIMON, M. and

VENTER, J.C.

TITLE Use of a random human BAC End Sequence Database for Sequence-Ready
 Map Building
 JOURNAL Unpublished (1998)
 COMMENT Other-GSS: CITBI-EI-2516A7.TF
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdamad@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tdb/humgen/BAC_end_search/BAC_end_search.html.
 Seq primer: M13-21
 Class: BAC ends

FEATURES
 Location/Qualifiers

1..310
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2516A7"
 /clone.lib="CITBI-EI"
 /sex="male"
 /cell_type="sperm"
 /note="Vector: pBelobAC11, Site_1: EcoRI; Site_2: EcoRI;
 Caltech Human BAC Library D"
 BASE COUNT 75 a 77 c 88 t 1 others
 ORIGIN

Query Match 32.6%; Score 293; DB 13; Length 310;
 Best Local Similarity 96.5%; Pred. No. 3.5e-53;
 Matches 299; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

368 ccaagctgtccatgagtgatccctggtgtctctgctatgatactgattctgtctt 427
 |||||||
 1 CCAGCTGTCCATGATGATCCGCGGCTCTGCTATGATGATGATGATGATGATGATG 60
 |||||||
 428 tccatagaaatatacagtgcttatactgctccatctctcctaagaaattctctccaa 487
 |||||||
 61 TCCATAGCAAAATATGACAGGTTTATGATGATGATGATGATGATGATGATGATG 120
 |||||||
 488 atgcacaaatcacaagaatgatactgctgctatacagaattctctctctctctc 547
 |||||||
 121 ATGCCCAATTCAAAAGACATACACGCTGCTATGATGATGATGATGATGATGATG 180
 |||||||
 548 tctcagtcacattgcttctctctctctctctctctctctctctctctctctctc 607
 |||||||
 181 TCTCAGTGCATTTCTTATCTTCTTTTCTGATATGCTCTAGATTTATCTCTCTG 240
 |||||||
 608 ggcacaccgcaaaatgaaacacagtgccgcaagaggtctctctgcaagggtgac 667
 |||||||
 241 GGCACACCCGCCCAATGAAACACAGCGCGCGGACGAGGCTTCTGACAGGGTGCAC 300
 |||||||
 668 ccatacagc 677
 |||||||
 301 CCATCAGCGC 310
 |||||||

RESULT 6

LOCUS BG192000 261 bp mRNA EST 21-APR-2001
 DEFINITION RST1106 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.

ACCESSION BG192000
 VERSION BG192000.1 GI:13713687
 KEYWORDS EST

SOURCE

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 261)

REFERENCE

HARRINGTON, J.J., SHERF, B., RUNDLETT, S., JACKSON, P.D., PERRY, R.,

CAHN, S., DAHL, T., THORNTON, M., RAMACHANDRAN, R., WHITTINGTON, J.,

Veloso, N., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J., and Ducar, M.

TITLE

Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression

JOURNAL

Nat. Biotechnol. 19 (3), 440 (2001) In press

COMMENT

Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com
High quality sequence stop: 321.
Location/Qualifiers
1. .321

FEATURES

SOURCE

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 96 a 59 c 54 g 112 t
ORIGIN

Query Match 24.8%; Score 223.2; DB 11; Length 321;
Best Local Similarity 98.3%; Pred. No. 3.8e-38;
Matches 236; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Oy 42 gacaaatctctctctggaatcttcacaaatgacatctggtggtggaatgacatga 101
|||||
Db 6 CATACAAATTTCTTCTGTGA-TTTCAGCAATGCGATCTTGTGGCGAATGCGATTGA 64

Oy 102 ctgacacagacagaaatgagtcgcgtgcatccctctctctctctgacgttc 161
|||||
Db 65 CTGATTAAGACAGAAATAGCGCTCCGCTGAGTCTCTCTCTCTCTGCGAGTTTC 124

Oy 162 tagaatctctctgacgtgtgtcatctctctacgttaatgagtgatctctctcataga 221
|||||
Db 125 TACGAATTTTCTGCGAGTTCATCTTACCTTAATGTGATCTTATCTTCAATAGCA 184

Oy 222 attcattcgtctgacgaatctgcaatctctctctctctctctctctctctgacgttc 281
|||||
Db 185 ATTCAATCTGCTTCTGCGAATGCGAATCTCTTATTATTAATGAATGGAATCTTG 244

RESULT 9

AL037695 554 bp mRNA EST 29-FEB-2000
LOCUS DKF256400672.1 564 (synonym: hfb2) Homo sapiens cDNA clone
DEFINITION DKF256400672.1, mRNA sequence.

ACCESSION AL037695
VERSION AL037695.3 GI:5928268
KEYWORDS EST.

SOURCE

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 554)
AUTHORS Blum, H., Bauerachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Blum, et al.)
JOURNAL Unpublished (1999)
COMMENT On Jul 7, 1999 this sequence version replaced gi:5865546.
Contact: Blum H

MIS

Am Klopferpitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de,
sequenced by LMU (Ludwig Maximilians University,

Munich/Germany) within the cDNA sequencing consortium of the German Genome Project.

s1 sequence also available.

This clone (DKF256400672) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

SOURCE

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="DKF256400672"
/clone_lib="564 (synonym: hfb2)"
/tissue_type="brain"
/dev_stage="fetal"
/lab_host="X1-2plue"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

BASE COUNT 154 a 96 c 108 g 196 t
ORIGIN

Query Match 8.9%; Score 80.2; DB 10; Length 554;
Best Local Similarity 48.9%; Pred. No. 2.2e-07;
Matches 250; Conservative 0; Mismatches 253; Indels 8; Gaps 1;

Oy 22 atcattctctctgagtgatatacaatctctctctgagatcttcacaaatgacatc 81
|||||
Db 5 ATTATTAATTAATTTCTGATGTTGATTTGTTCTGGAATGTTGCAATGCTTCATA 64

Oy 82 gtggtgtgaaatgagatctgacatctgacatcaagacagaaatgagtcgcgtgacatc 141
|||||
Db 65 GCTTATTAATTAATTTCTGATGTTGATTTGTTCTGGAATGTTGCAATGCTTCATA 124

Oy 142 ctctctctgagatcttcagat-----cttctgacgtcttctctctctcag 193
|||||
Db 125 GTCACTGCTCTGCGATCTTCCAGAAATGTTGTTGATTTGATTTATTAATTTGATG 184

Oy 194 ttaatgagatcttc 253
|||||
Db 185 CAAGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 244

Oy 254 tctattataaagaatctggaatctgacatctgacatctgacatctgacatctgacat 313
|||||
Db 245 CGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTCT 304

Oy 314 ccaaggtctgacagcgtccgacacacatctctctctctctctctctctctctctc 373
|||||
Db 305 TCAGATTTGCAATTTCTCAATTTATTTATTTCTGCAATTAAGAAATTAAGATG 364

Oy 374 tggctcagatgacatc 433
|||||
Db 365 TTTCTTCTGATTAATTTCTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 424

Oy 434 gcaaatatgaggtgtctgacatctctctctctctctctctctctctctctctc 493
|||||
Db 425 CCAATGCGATGACAGTGTGTTGACAAAGAAATTTGAAGCAATGTTGATTTGATTT 484

Oy 494 caattcaaaagaagatgacatctctctctctctctctctctctctctctctc 524
|||||
Db 485 GAATGAGGAATGCAATACACCTTTCAACAA 515

RESULT 10

AQ103952 383 bp DNA GSS 28-AUG-1998
LOCUS HS_3107_AL_C05_T7 CIT Approved Human Genomic Sperm Library D Homo
DEFINITION HS_3107_AL_C05_T7 CIT Approved Human Genomic Sperm Library D Homo

ACCESSION AQ103952
VERSION AQ103952.1 GI:3478888
KEYWORDS GSS.

SOURCE

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

COMMENT	<p>Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu</p> <p>Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Plerer de Jong (plererdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (http://www.hnsc.washington.edu). BAC end Web Server: http://www.hnsc.washington.edu</p> <p>Plate: 976 row: M column: 7 Seq primer: 77 Class: BAC ends High quality sequence stop: 589.</p>
FEATURES	<p>Location/Qualifiers</p> <p>1..589</p> <p>/organism="Homo sapiens" /db_xref="taxon:9606" /clone="plate=976 Col=7 Row=M" /clone_1id="RPCI-11 Human Male BAC Library" /sex="male" /note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRII Methyase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"</p>
BASE COUNT	166 a 98 c 117 g 199 t 9 others
ORIGIN	
Query Match	6.0%; Score 53.8; DB 13; Length 589;
Best Local Similarity	60.7%; Pred. No. 0.11;
Matches 102; Conservative	0; Mismatches 65; Indels 1; Gaps 1
OY	1 atgcgagatcctccaccattactcttcttcgtcgagatacaattctcttgagg 60
DJ	311 ATGATGTGTTTTCCTCATCATCATTAATCAATTGGTAGAGATTGC -ATTGTGTTTGGA 369
OY	61 attccaacaatggacalcattgctgctggaatggcatgatgcatgacgacaga 120
DJ	370 AATGTGCCAATGAGCTTCATAGCTCAGTAATGTGCTATGACTGNGTTAACACGAGAAG 429
OY	121 atggctccgctgatatctctctttcttcgtcgcagttcttagaat 168
DJ	430 ATCTCTCAGCTGAGCAAAATCTCACCTGCTCGTGGTCTCCAGAAAT 477
RESULT 12	AZ739176 787 bp DNA GSS 25-JAN-2001
LOCUS	AZ739176/c
DEFINITION	RPCI-24-154D22.TV RPCI-24 mus musculus genomic clone RPCI-24-154D22
ACCESSION	'DNA sequence.'
VERSION	AZ739176
KEYWORDS	AZ739176.1 GI:12509031
SOURCE	GSS.
ORGANISM	house mouse. Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 787) Zhao,S., Nieman,M., Malek,J., Shatsman,S., Akhmet,B., Levins,M., Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
TITLE	Mouse BAC end Sequences from Library RPCI-24
JOURNAL	Unpublished (1999)
COMMENT	Other_GSSs: RPCI-24-154D22.TJ Contact: Shaying Zhao Department of Eukaryotic Genomics, The Institute for Genome Sciences and Policy,

COMMENT	FEATURES	BASE COUNT	ORIGIN
<p>Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu</p> <p>Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Plerer de Jong (plerer@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (Inforesgen.com). BAC end Web Server: http://www.hnsc.washington.edu</p> <p>Plate: 976 row: M column: 7 Seq primer: 77 Class: BAC ends High quality sequence stop: 589.</p>	<p>Location/Qualifiers</p> <p>1. 589</p> <p>/organism="Homo sapiens" /db_xref="taxon:9606" /clone="Plate=976 Col=7 Row=M" /clone_11b="RPCI-11 Human Male BAC Library" /sex="male" /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRII. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"</p>	<p>166 a 98 c 117 g 199 t 9 others</p>	<p>Query Match</p> <p>Best Local Similarity 60.7%; Score 53.8; DB 13; Length 589; Matches 102; Conservative 0; Mismatches 65; Indels 1; Gaps 1</p>
<p>RESULT 12 LOCUS A2739176/c DEFINITION RPCI-24-154D22.TV RPCI-24 musculus genomic clone RPCI-24-154D22 ACCESSION A2739176 VERSION A2739176.1 GI:12509031 SOURCE GSS. ORGANISM Mus musculus house mouse. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus. 1 (bases 1 to 787) Zhang, S., Nieman, M., Malek, J., Shatsman, S., Akhmet, B., Levins, M., Russell, D., de Jong, P., and Fraser, C.M. Mouse BAC end Sequences from Library RPCI-24 Unpublished (1999) Other_GSSs: RPCI-24-154D22.TV Contact: Shaying Zhao Department of Eukaryotic Genomics, The Institute for Genome Sciences and</p>	<p>1 atgcgagagctcaaccctcattctatcttctcttcgacgatacaattctcttcg 60 db 311 ATGATGCTGTTCCTGCTCATCATCATTAATCAATTCAGTAAGATTCC-ATTTGTTCTTGA 369 61 atttccaaatgacalcattcgtcgtcgtgaatgacattgacattgacacagcaaa 120 db 370 AATGTNCCCAATGAGCTTCATAGCTGTAAGTAATGTCATTGACTGNGTTAACACAGCAAG 429 0y 121 atggctccgctgatatctctctctctctctctctctctctctctctctctct 168 db 430 ATCTCTCAGCTGAGCAAAATCTCATCTGCTGCTGCTCCAGAAAT 477</p>	<p>787 bp DNA GSS 25-JAN-2001 A2739176 ' DNA sequence. A2739176 A2739176.1 GI:12509031 GSS. house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus. 1 (bases 1 to 787) Zhang, S., Nieman, M., Malek, J., Shatsman, S., Akhmet, B., Levins, M., Russell, D., de Jong, P., and Fraser, C.M. Mouse BAC end Sequences from Library RPCI-24 Unpublished (1999) Other_GSSs: RPCI-24-154D22.TV Contact: Shaying Zhao Department of Eukaryotic Genomics, The Institute for Genome Sciences and</p>	

Tue Dec 11 09:54:25 2001

us-09-510-332-2.ts